```
              :|::||:|  :      ||    :  :|:  |||:|:  | ||| :   :    |  |:|
Db         79 ETSFVFYDGSLTASYKDRATSYPQ-GIKLNQVTRKDAGEYSCEVTSTGTKVLYGEAKIQL 137

Qy        134 TVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNS 193
              | | | ||| :|| :   | :| | | |::| | | ::|| |: |:   |       :||
Db        138 QVIVAPGTPVAQVPSSARTGSVAELMCVETQGFPLPTFTWYHNNSPMQAKS------QNS 191

Qy        194 SSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGGVLVVL 253
              :  ::  || | | :|   |||:||| |:|  |         :| |:|:|||:  |::||
Db        192 TYTIDPNTGVLKFASVGTSDSGEYYCKATNSQGEQSSAIVRMDVKDVNVGGIVAAVVIVL 251

Qy        254 AVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
              :|||:  |:  || |||          |  | :        |  : :|:  |||::
Db        252 LILALLGFGLWFAYSRGYLDRKGNKKVIYSQPSE--------TRSDKNFQQTSSFLV 300


RESULT 14
Q9Y5B2
ID   Q9Y5B2      PRELIMINARY;      PRT;   259 AA.
AC   Q9Y5B2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction adhesion molecule.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liu Y., Nusrat A., Schnell F.J., Walsh S., Reaves T.A., Pochet M.,
RA   Foley C., Parkos C.A.;
RT   "Human junctional adhesion molecule is expressed by polarized columnar
RT   epithelia and regulates tight junction resealing.";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF154005; AAD43794.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   259 AA;  28122 MW;  FE38521A911582D0 CRC64;

  Query Match             20.2%;  Score 331;  DB 4;  Length 259;
  Best Local Similarity   29.6%;  Pred. No. 4.8e-24;
  Matches   81;  Conservative   44;  Mismatches  111;  Indels   38;  Gaps    7;

Qy         42 VVQEFESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLK 101
              ::  |   |:|||    |  | ||       ::: |::                | :
Db         19 ILPENNPVKLSCAY--SGFSSPR---AASYEDRVTFL-----------------PTGIT 55

Qy        102 IWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQ 161
              :||| |:  | | :|       |: ::| | | |   :| :  :|  | | |
Db         56 FKSVTREDTGTYTC-MVFEEGGNSYGEVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCS 114

Qy        162 ESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIA 221
              | :| |   |:|::: : :||: ::   | |||  ||  || |||  :   |:|:| | |
Db        115 EQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEA 174

Qy        222 SNDAGSARCEEQ-EMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGE 280
              |  |:         ||  : |:| |:  ||| | :| ::  ||  || ||:|   |:
Db        175 RNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTS 234

Qy        281 S----YKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
              |    |  |             ||:|:  |||::
Db        235 SKKVIYSQPS---------ARSEGEFKQTSSFLV 259


RESULT 15
Q9JKD5
ID   Q9JKD5      PRELIMINARY;      PRT;   173 AA.
AC   Q9JKD5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junctional adhesion molecule (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kirsch T., Wellner M., Haller H., Lippoldt A.;
RT   "Cloning of the rat junctional adhesion molecule (JAM).";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF241261; AAF61729.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain.
FT   NON_TER       1      1
SQ   SEQUENCE   173 AA;  18706 MW;  3EE3ECDFA5AFB8B2 CRC64;

  Query Match             19.6%;  Score 321;  DB 11;  Length 173;
  Best Local Similarity   40.3%;  Pred. No. 2.7e-23;
  Matches   71;  Conservative   27;  Mismatches   72;  Indels    6;  Gaps    3;

Qy        137 VKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT-DSRANPRFRNSSS 195
              | |  |   :| :| :|  | | | | :| |   |||::: ||: | |::    | |||
Db          2 VPPSKPTVSIPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGVPMLTADAKKTRAFINSSY 61

Qy        196 HLNSETGTLVFTAVHKDDSGQYYCIASNDAGSA-RCEEQEMEVYDLNIGGIIGGVLVVLA 254
              :: ::| |||  |   |||:||| | |  |:| | |   ||  :||:|||:  ||| |
Db         62 TIDPKSGDLVFDPVSAFDSGEYYCEAQNGYGTAMRSEAVRMEAVELNVGGIVAAVLVTLI 121

Qy        255 VLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
              :| |:  ||  || ||||   |:       |||    :       ||:|:  |||::
Db        122 LLGLLIFGIWFAYSRGYFERTKKG----TAPGKKVIYSQPSARSEGEFKQTSSFLV 173


Search completed: April 12, 2004, 09:16:12
Job time : 47 secs
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Qy          83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTP 142
               :      || |     : :  :||:|:  | ||| :   :     |  |:| | | |  |
Db          77 SLTAPYKDRA-IPYPQGITLKQITRKDAGEYSCEVTSTGSKTLYGEAKIQLQVIVAPSKP 135

Qy         143 VCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLNSETG 202
               | :||::|  | :| | | |::|:| | : |||| |:    :  |  :||:  :: :||
Db         136 VAQVPRSVSTGSVAELLCVENDGYPPPTFIWYRNKSPM----QIAP--QNSTYTIDPKTG 189

Qy         203 TLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGGVLVVLAVLALITLG 262
               | | ||   |||:||| |:|: |    :   |:| |:|:|||:  |::|| :|||| |
Db         190 VLKFAAVSTSDSGEYYCEATNNQGKQASDLVRMDVQDVNVGGIVAAVVIVLLILALIGFG 249

Qy         263 ICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
               :  || |||   :     |  | :       |  : :|:  |||::
Db         250 MWFAYSRGYLDRKENKKVIYSLPSE--------TRSDKNFQQTSSFLV 289


RESULT 12
Q8VC39
ID   Q8VC39      PRELIMINARY;      PRT;   300 AA.
AC   Q8VC39;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Junction cell adhesion molecule1).
GN   F11R.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Cecum;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; BC021876; AAH21876.1; -.
DR   EMBL; AK033574; BAC28369.1; -.
DR   MGD; MGI:1321398; F11r.
DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   300 AA;  32423 MW;  3CE561E8FF3B97EC CRC64;

  Query Match             27.5%;  Score 449.5;  DB 11;  Length 300;
  Best Local Similarity   35.2%;  Pred. No. 1.3e-35;
  Matches  105;  Conservative   56;  Mismatches  122;  Indels   15;  Gaps    7;

Qy          20 LLLLFRGCLIGAV-----NLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEWKKIQDEQ 74
               ||  ||    ::|::     :: ::     | | ||::|:|  | |  | ||:||| :|
Db          11 LLFLFTSMILGSLVQGKGSVYTAQSDVQVPENESIKLTC--TYSGFSSPRVEWKFVQGST 68

Qy          75 TTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELT 134
               |  | ::::|    | |      : :   :|||:|:  | | :|:    :    |: | ||
Db          69 TALVCYNSQITAPYADRV-TFSSSGITFSSVTRKDNGEYTC-MVSEEGGQNYGEVSIHLT 126

Qy         135 VQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT-DSRANPRFRNS 193
               | | |  |  || :| :|  | | | | :| |  |||::: : : | |::   | ||
Db         127 VLVPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNS 186

Qy         194 SSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSA-RCEEQEMEVYDLNIGGIIGGVLVV 252
               |  :: ::| |:|  |   |||:||| | |  |:| | |    |:  :||:|||:  |||
Db         187 SFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGIVAAVLVT 246

Qy         253 LAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
               | :| |:  |:  || ||||   |:       |||    :   |  ||:|:  |||::
Db         247 LILLGLLIFGVWFAYSRGYFERTKKG----TAPGKKVIYSQPSTRSEGEFKQTSSFLV 300


RESULT 13
Q7SYQ7
ID   Q7SYQ7      PRELIMINARY;      PRT;   300 AA.
AC   Q7SYQ7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   MEDLINE=22341132; PubMed=12454917;
RA   Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA   Richardson P.;
RT   "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT   initiative.";
RL   Dev. Dyn. 225:384-391(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Whole;
RA   Klein S., Strausberg R.;
RL   Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC054305; AAH54305.1; -.
KW   Hypothetical protein.
FT   NON_TER       1       1
SQ   SEQUENCE   300 AA;  32858 MW;  02BC49DC74E271D4 CRC64;

  Query Match             26.6%;  Score 435.5;  DB 13;  Length 300;
  Best Local Similarity   34.7%;  Pred. No. 3.1e-34;
  Matches  103;  Conservative   54;  Mismatches  115;  Indels   25;  Gaps    7;

Qy          20 LLLLFRGCLIGA--VNLKSSNRTPVVQEFESVELSCIITDSQTSD---PRIEWKKI-QDE 73
               | ||   ||  |    : : : |  |:| :| :| |    | |||   ||:||| : :|:
Db          23 LALLCCCCLWTAALAGVTAPDPTITVKEGDSPDLRC----SYTSDYINPRVEWKFVNKDQ 78

Qy          74 QTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIEL 133
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DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction cell adhesion molecule 2.
GN   JAM2 OR JCAM2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Skin;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK028757; BAC26102.1; -.
DR   MGD; MGI:1933820; Jam2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   298 AA;  33079 MW;  CB8227EC13D349A3 CRC64;

  Query Match             29.3%;  Score 478.5;  DB 11;  Length 298;
  Best Local Similarity   36.3%;  Pred. No. 1.8e-36;
  Matches  113;  Conservative   54;  Mismatches  117;  Indels   27;  Gaps    9;

Qy         13 ARLPDFFLLLLFRGCLIGAVNLKSSN---------RTPVVQEFESVELSCIITDSQTSDP 63
              ||  |    |:||    || |::   :|         :   | ||:   |:|  |  :|:
Db          2 ARSPQGLLMLLLLHYLIVALDYHKANGFSASKDHRQEVTVIEFQEAILAC-KTPKKTTSS 60

Qy         64 RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDR 123
              |:||||:  :  : |::   :|||   |||::   :::| |||| |: |||||  |  ::
Db         61 RLEWKKV-GQGVSLVYYQQALQGDFKDRAEMI-DFNIRIKNVTRSDAGEYRCEVSAPTEQ 118

Qy        124 -KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT 182
               : :  |  :  | | : |  | | ||| :|   |  :   | ||: ||:| | |  |:::     |
Db        119 GQNLQEDKVMLEVLMAPAVPACEVPTSVMTGSVVELRCQDKEGNPAPEYIWFKDG----T 174

Qy        183 DSRANPR---FRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYD 239
                 ||:    |||  :|:::| | |  : | |||:||| | |  |  ||  : |:|
Db        175 SLLGNPKGGTHNNSSYTMNTKSGILQFNMISKMDSGEYYCEARNSVGHRRCPGKRMQVDV 234

Qy        240 LNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEE 299
              ||| |||  |:||  |::: || | | |:|||       |:    | |   : : |  |
Db        235 LNISGIIATVVVVAFVISVCGLGTCYAQRKGYF-----SKETSFQKGSP--ASKVTTMSE 287

Qy        300 GDFRHKSSFVI 310
               ||:|  ||:|
Db        288 NDPKHTKSFII 298


RESULT 10
Q9JHY1
ID   Q9JHY1      PRELIMINARY;      PRT;   300 AA.
AC   Q9JHY1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junctional adhesion molecule JAM.
GN   JAM.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague Dawley;
RA   Mashima H., Kojima I.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF276998; AAF78250.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   300 AA;  32369 MW;  45AE362A96158BFA CRC64;

  Query Match             28.0%;  Score 458.5;  DB 11;  Length 300;
  Best Local Similarity   37.9%;  Pred. No. 1.7e-36;
  Matches  113;  Conservative   48;  Mismatches  122;  Indels   15;  Gaps    8;

Qy         20 LLLLFRGCLIGA-VNLKSSNRTP----VVQEFESVELSCIITDSQTSDPRIEWKKIQDEQ 74
              || ||   ::|: |  | |  :|      | | :||:| ||   | | ||:||| :|
Db         11 LLFLFTSMILGSLVQGKGSVYSPQTAVQVPENDSVKLPCIY--SGFSSPRVEWKFVQGST 68

Qy         75 TTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELT 134
              |  | ::|:|    | |       : :   :|||:|:  | | :|: :  :    |: | ||
Db         69 TALVCYNNQITVPYADRV-TFSSSGITFSSVTRKDNGEYTC-MVSEDGGQNYGEVSIHLT 126

Qy        135 VQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT-DSRANPRFRNS 193
              | | |   |   :| :| :|  | | | | :| |   |||::: ||: | |::    | ||
Db        127 VLVPPSKPTVSIPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGVPMLTADAKKTRAFINS 186

Qy        194 SSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSA-RCEEQEMEVYDLNIGGIIGGVLVV 252
              |  :: ::| |||  |   |||:||| | |  |:| | |   ||  :||:|||:  |||
Db        187 SYTIDPKSGDLVFDPVSAFDSGEYYCEAQNGYGTAMRSEAVRMEAVELNVGGIVAAVLVT 246

Qy        253 LAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
              | :| |:  ||  || ||||   |:        |||    :       ||:|:  |||::
Db        247 LILLGLLIFGIWFAYSRGYFERTKKG----TAPGKKVIYSQPSARSEGEFKQTSSFLV 300


RESULT 11
Q7ZWT0
ID   Q7ZWT0      PRELIMINARY;      PRT;   289 AA.
AC   Q7ZWT0;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to junctional adhesion molecule 1.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Strausberg R.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC046720; AAH46720.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   289 AA;  31630 MW;  24354B5A37618845 CRC64;

  Query Match             27.8%;  Score 455;  DB 13;  Length 289;
  Best Local Similarity   35.8%;  Pred. No. 3.6e-36;
  Matches  103;  Conservative   56;  Mismatches  109;  Indels   20;  Gaps    7;

Qy         27 CLIGAVNL---KSSNRTPVVQEFESVELSCIITDSQTSDPRIEWKKI-QDEQTTYVFFDN 82
              | :  | |    : | | :|:| || || |  :   || ||:||| : :|::|::||:|
Db         18 CCLWTVTLAAVTTPNPTIIVKEGESAELQCSYSSDFTS-PRVEWKFVNKDQETSFVFYDG 76
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RC   STRAIN=C57BL/6J;
RX   MEDLINE=20317114; PubMed=10779521;
RA   Palmeri D., van Zante A., Huang C.-C., Hemmerich S., Rosen S.D.;
RT   "Vascular Endothelial Junction-associated Molecule, a Novel Member of
RT   the Immunoglobulin Superfamily, Is Localized to Intercellular
RT   Boundaries of Endothelial Cells.";
RL   J. Biol. Chem. 275:19139-19145(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   PubMed=11036763;
RA   Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT   "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT   Family?";
RL   Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo, and Embryonic stem cells;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AF255911; AAF81224.1; -.
DR   EMBL; AJ291757; CAC20699.1; -.
DR   EMBL; AK013914; BAB29053.1; -.
DR   EMBL; AK010616; BAB27064.1; -.
DR   MGD; MGI:1933820; Jam2.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   298 AA;  33047 MW;  1124E0F07E6CF751 CRC64;

  Query Match             29.4%;  Score 481.5;  DB 11;  Length 298;
  Best Local Similarity   36.7%;  Pred. No. 9.3e-39;
  Matches  114;  Conservative   53;  Mismatches  117;  Indels   27;  Gaps    9;

Qy         13 ARLPDFFLLLLFRGCLIGAVNLKSSN---------RTPVVQEFESVELSCIITDSQTSDP 63
              ||  |   |:||    || |::  :|         :   | ||:   |:|  |  :|:
Db          2 ARSPQGLLMLLLLHYLIVALDYHKANGFSASKDHRQEVTVIEFQEAILAC-KTPKKTTSS 60

Qy         64 RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDR 123
              |:||||:  :  : |::   :|||   |||::   :::| ||||  |:  |||||  |  ::
Db         61 RLEWKKV-GQGVSLVYYQQALQGDFKDRAEMI-DFNIRIKNVTRSDAGEYRCEVSAPTEQ 118

Qy        124 -KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT 182
               : :|  : | | |  | | || :|  | :  | ||: ||:| | | |:::    |
Db        119 GQNLQEDKVMLEVLVAPAVPACEVPTSVMTGSVVELRCQDKEGNPAPEYIWFKDG----T 174

Qy        183 DSRANPR---FRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYD 239
                 ||:    |||  :|:::| | |  : | ||||:||| | |  |  ||  : |:|
Db        175 SLLGNPKGGTHNNSSYTMNTKSGILQFNMISKMDSGEYYCEARNSVGHRRCPGKRMQVDV 234

Qy        240 LNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEE 299
              ||| |||  |:||  |:::  || | | |:|||       |:    | |   : : | |
Db        235 LNISGIIATVVVVAFVISVCGLGTCYAQRKGYF-----SKETSFQKGSP--ASKVTTMSE 287

Qy        300 GDFRHKSSFVI 310
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              ||:|  ||:|
Db        288 NDFKHTKSFII 298


RESULT 8
Q8C5K9
ID   Q8C5K9      PRELIMINARY;      PRT;   298 AA.
AC   Q8C5K9;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction cell adhesion molecule 2.
GN   JAM2 OR JCAM2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK078128; BAC37139.1; -.
DR   MGD; MGI:1933820; Jam2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   298 AA;  33182 MW;  1131F0BFD89CEB51 CRC64;

  Query Match             29.4%;  Score 481.5;  DB 11;  Length 298;
  Best Local Similarity   37.0%;  Pred. No. 9.3e-39;
  Matches  115;  Conservative   53;  Mismatches  116;  Indels   27;  Gaps    9;

Qy         13 ARLPDFFLLLLFRGCLIGAVNLKSSN---------RTPVVQEFESVELSCIITDSQTSDP 63
              ||  |   |:||    || |::  :|         :   | ||:   |:|  |  :|:
Db          2 ARSPQGLLMLLLLHYLIVALDYHKANGFSASKDHRQEVTVIEFQEAILAC-KTPKKTTSS 60

Qy         64 RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDR 123
              |:||||:  :  : |::   :|||   |||::   :::| ||||  |:  |||||  |  ::
Db         61 RLEWKKV-GQGVSLVYYQQALQGDFKDRAEMI-DFNIRIKNVTRSDAGEYRCEVSAPTEQ 118

Qy        124 -KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT 182
               : :|  : | | |  | | || :|  | :  | ||: ||:| | | |:::    |
Db        119 GQNLQEDKVMLEVLVAPAVPACEVPTSVMTGSVVELRCQDKEGNPAPEYIWFKDGHSL-- 176

Qy        183 DSRANPRFR---NSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYD 239
                 ||:  |   |||  :|:::| | |  : | |||:||| | |  |  ||  : |:|
Db        177 --LGNPKGRTHNNSSYTMNTKSGILQFNMISKMDSGEYYCEARNSVGHRRCPGKRMQVDV 234

Qy        240 LNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEE 299
              ||| |||  |:||  |:::  || | | |:|||       |:    | |   : : | |
Db        235 LNISGIIATVVVVAFVISVCGLGTCYAQRKGYF-----SKETSFQKGSP--ASKVTTMSE 287

Qy        300 GDFRHKSSFVI 310
              ||:|  ||:|
Db        288 NDFKHTKSFII 298


RESULT 9
Q8CE95
ID   Q8CE95      PRELIMINARY;      PRT;   298 AA.
AC   Q8CE95;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
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RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Mesonephros;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AJ300304; CAC20704.1; -.
DR   EMBL; AK013156; BAB28683.1; -.
DR   EMBL; BC024357; AAH24357.1; -.
DR   EMBL; AK032833; BAC28049.1; -.
DR   MGD; MGI:1933825; Jam3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34837 MW;  4B92BCB51D0A4B0A CRC64;

  Query Match             86.5%;  Score 1415;  DB 11;  Length 310;
  Best Local Similarity   86.1%;  Pred. No. 1.6e-130;
  Matches  267;  Conservative   18;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||| |  |||| |||||||||||||||:| |||||||||| ||| ||||||||||||||||
Db          1 MALSRRLRLRLYARLPDFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| ||||||:||||||||||||||
Db        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||:||| |:||||||||| ||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 6
Q9D1M9
ID   Q9D1M9      PRELIMINARY;      PRT;   310 AA.
AC   Q9D1M9;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   1110002N23Rik protein.
GN   JCAM3 OR JCAM2 OR 1110002N23RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK003326; BAB22715.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
SQ   SEQUENCE   310 AA;  34819 MW;  6692BCAD68EA4B1D CRC64;

  Query Match             85.8%;  Score 1403;  DB 11;  Length 310;
  Best Local Similarity   85.2%;  Pred. No. 2.5e-129;
  Matches  264;  Conservative   20;  Mismatches   26;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||| |  |||| |||||||||||||||:| |||||||||| ||| ||||||||||||||||
Db          1 MALSRRLRLRLYARLPDFFLLLLFRGCMIEAVNLKSSNRNPVVHEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              |||||||||||| |||||:|||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              |||||:||| ||| ||||||||||:| |||||| ||| ||||||:||||||||||||||
Db        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||:||| |:||||||||| ||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| |||||||| |||
Db        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300

Qy        301 DFRHKSSFVI 310
              ||:|| :|||
Db        301 DFKHKIAFVI 310


RESULT 7
Q9JI59
ID   Q9JI59      PRELIMINARY;      PRT;   298 AA.
AC   Q9JI59;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Vascular endothelial junction-associated molecule (Junctional adhesion
DE   molecule-3) (2410030G21Rik protein).
GN   JAM2 OR JCAM3 OR JCAM2 OR JAM-3 OR 2410030G21RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
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Qy          2 ALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS 61
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS 60

Qy         62 DPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARN 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARN 120

Qy        122 DRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLP 181
              ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DRKEIDEIVIELTVRVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLP 180

Qy        182 TDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLN 241
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLN 240

Qy        242 IGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGD 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 IGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGD 300

Qy        302 FRHKSSFVI 310
              |||||||||
Db        301 FRHKSSFVI 309
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RESULT 4
Q9D8B7
ID Q9D8B7 PRELIMINARY; PRT; 310 AA.
AC Q9D8B7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1110002N23Rik protein.
GN JCAM3 OR JCAM2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008187; BAB25519.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain.
SQ SEQUENCE 310 AA; 34855 MW; C74884EABE234680 CRC64;

  Query Match 86.7%; Score 1417; DB 11; Length 310;
  Best Local Similarity 86.1%; Pred. No. 1e-130;
  Matches 267; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

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Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||| |  |||| |||||||||||||||:| |||||||| ||||||||||||||||||||
Db          1 MALSRRLRLRLYARLPDFFLLLLFRGCMIEAVNLKSSNRNPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              |||||||||||| |||||:|||||||||||||| :: |||||:|||||| |||:|||||||
Db         61 SDPRIEWKKIQDGQTTYVYFDNKIQGDLAGRTDVFGKTSLRIWNVTRSDSAIYRCEVVAL 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              |||||:||| ||| |||||||||||:| |||||| ||| |||||:|||||:||||||||
Db        121 NDRKEVDEITIELIVQVKPVTPVCRIPAAVPVGKTATLQCQESEGYPRPHYNWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||:||| |:|||||||| ||||||||||||||||||:|||| |:||||||
Db        181 PTDSRANPRFQNSSFHVNSETGTLVFNAVHKDDSGQYYCIASNDAGAARCEGQDMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              || |||||||||| |||:||:|||||||| ||::|||||||:||| ||||||| |||
Db        241 NIAGIIGGVLVVLIVLAVITMGICCAYRRGCFISSKQDGESYKSPGKHDGVNYIRTSEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 5
Q9EPK4
ID Q9EPK4 PRELIMINARY; PRT; 310 AA.
AC Q9EPK4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule-2, JAM-2 (1110002N23Rik protein)
DE (Junction cell adhesion molecule 3).
GN JAM3 OR JCAM3 OR JCAM2 OR JAM-2 OR 1110002N23RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11036763;
RA Aurrand-Lions M.A., Duncan L., Du Pasquier L., Imhof B.A.;
RT "Cloning of JAM-2 and JAM-3: an Emerging Junctional Adhesion Molecular
RT Family?";
RL Curr. Top. Microbiol. Immunol. 251:91-98(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:12:08 ; Search time 45 Seconds
(without alignments)
2173.570 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 1635
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1629	99.6	310	4	Q9BX67	Q9bx67 homo sapien
2	1629	99.6	355	4	Q8WWL8	Q8wwl8 homo sapien
3	1620	99.1	309	4	Q96FL1	Q96fl1 homo sapien
4	1417	86.7	310	11	Q9D8B7	Q9d8b7 mus musculu
5	1415	86.5	310	11	Q9EPK4	Q9epk4 mus musculu
6	1403	85.8	310	11	Q9D1M9	Q9d1m9 mus musculu
7	481.5	29.4	298	11	Q9JI59	Q9ji59 mus musculu
8	481.5	29.4	298	11	Q8C5K9	Q8c5k9 mus musculu
9	478.5	29.3	298	11	Q8CE95	Q8ce95 mus musculu
10	458.5	28.0	300	11	Q9JHY1	Q9jhy1 rattus norv
11	455	27.8	289	13	Q7ZWT0	Q7zwt0 xenopus lae
12	449.5	27.5	300	11	Q8VC39	Q8vc39 mus musculu
13	435.5	26.6	300	13	Q7SYQ7	Q7syq7 xenopus lae
14	331	20.2	259	4	Q9Y5B2	Q9y5b2 homo sapien
15	321	19.6	173	11	Q9JKD5	Q9jkd5 rattus norv
16	291	17.8	64	11	Q8BT59	Q8bt59 mus musculu
17	248	15.2	318	13	Q91664	Q91664 xenopus lae
18	242.5	14.8	304	11	Q9CVA4	Q9cva4 mus musculu
19	241	14.7	327	4	Q96IQ7	Q96iq7 homo sapien
20	239.5	14.6	284	4	Q9NX42	Q9nx42 homo sapien
21	239.5	14.6	325	4	O95791	O95791 homo sapien
22	232.5	14.2	328	11	Q9Z109	Q9z109 mus musculu
23	221.5	13.5	319	11	Q922D5	Q922d5 mus musculu
24	215.5	13.2	319	11	Q9JKA5	Q9jka5 mus musculu
25	215	13.1	407	11	Q9D2J4	Q9d2j4 mus musculu
26	209.5	12.8	335	13	Q9PWR4	Q9pwr4 gallus gall
27	209	12.8	181	13	Q91665	Q91665 xenopus lae
28	206.5	12.6	335	13	Q9YGH1	Q9ygh1 gallus gall
29	205.5	12.6	248	11	Q9D0T4	Q9d0t4 mus musculu
30	201.5	12.3	335	13	Q9YGV5	Q9ygv5 gallus gall
31	199.5	12.2	372	13	Q90Y50	Q90y50 brachydanio
32	198.5	12.1	387	4	Q86XK7	Q86xk7 homo sapien
33	197.5	12.1	373	4	Q9H6B4	Q9h6b4 homo sapien
34	193.5	11.8	795	13	Q90YM0	Q90ym0 brachydanio
35	189	11.6	259	4	Q7Z2Q1	Q7z2q1 homo sapien
36	187	11.4	725	13	O73633	O73633 xenopus lae
37	186.5	11.4	358	13	Q90490	Q90490 brachydanio
38	184.5	11.3	838	13	Q90YM1	Q90ym1 brachydanio
39	182.5	11.2	372	11	Q8K1G0	Q8k1g0 rattus norv
40	182.5	11.2	1409	13	Q8JI27	Q8ji27 brachydanio
41	182.5	11.2	1409	13	Q801M2	Q801m2 brachydanio
42	182.5	11.2	1428	13	Q8AY67	Q8ay67 brachydanio
43	180.5	11.0	1894	11	Q64487	Q64487 mus musculu
44	180	11.0	344	5	Q8WR42	Q8wr42 caenorhabdi
45	180	11.0	345	5	Q8MPV0	Q8mpv0 caenorhabdi

ALIGNMENTS

RESULT 1
Q9BX67
ID Q9BX67 PRELIMINARY; PRT; 310 AA.
AC Q9BX67;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Junctional adhesion molecule 3 precursor (Junctional adhesion
DE molecule-2) (Junctional adhesional molecule-3) (Hypothetical protein
DE FLJ90288) (Hypothetical protein FLJ90828).
GN JAM-2 OR JAM3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Cunningham S.A., Arrate M.P., Tran T.M.;
RT "Cloning of Human Junctional Adhesion Molecule 3.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.;
RT "Heterogeneity of endothelial junctions is reflected by differential
RT expression and specific subcellular localization of the three JAM
RT family members.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;
RT "Junctional adhesion molecules (JAMs) and interendothelial
RT junctions.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
RT "Characterization of Junctional Adhesional Molecule-3 on Human
RT Platelets· A New Member of Immunoglobulin Superfamily ";

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DR   HSSP; P12931; 1FMK.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   InterPro; IPR008266; Tyr_pkinase_AS.
DR   Pfam; PF00047; ig; 7.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00408; IGc2; 4.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50835; IG_LIKE; 7.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW   Receptor; Transmembrane; Signal; Glycoprotein; Cell adhesion;
KW   Immunoglobulin domain; Repeat.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23   1051       TYROSINE-PROTEIN KINASE-LIKE 7.
FT   DOMAIN       23    685       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    686    706       POTENTIAL.
FT   DOMAIN      707   1051       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       23    105       IG-LIKE C2-TYPE 1.
FT   DOMAIN      115    204       IG-LIKE C2-TYPE 2.
FT   DOMAIN      213    298       IG-LIKE C2-TYPE 3.
FT   DOMAIN      308    388       IG-LIKE C2-TYPE 4.
FT   DOMAIN      393    472       IG-LIKE C2-TYPE 5.
FT   DOMAIN      487    566       IG-LIKE C2-TYPE 6.
FT   DOMAIN      573    661       IG-LIKE C2-TYPE 7.
FT   DOMAIN      777   1048       PROTEIN KINASE; INACTIVE.
FT   DISULFID     40     88       BY SIMILARITY.
FT   DISULFID    137    187       BY SIMILARITY.
FT   DISULFID    234    282       BY SIMILARITY.
FT   DISULFID    326    372       BY SIMILARITY.
FT   DISULFID    414    462       BY SIMILARITY.
FT   DISULFID    505    551       BY SIMILARITY.
FT   DISULFID    594    645       BY SIMILARITY.
FT   CARBOHYD    103    103       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    202    202       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    255    255       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    264    264       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    444    444       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    548    548       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    627    627       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1051 AA;  116366 MW;  1752442AEA4CB702 CRC64;

  Query Match             10.1%;  Score 164.5;  DB 1;  Length 1051;
  Best Local Similarity   24.5%;  Pred. No. 6.9e-06;
  Matches   66;  Conservative   35;  Mismatches  109;  Indels   59;  Gaps   11;

Qy          40 TPVVQEFESVE------LSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAE 93
               ||  |  : :|       :||  |  :   | |:| |             : :   :: ||
Db         486 TPPPQPLQCMEFNKEVTVSCSATGRE--KPTIQWTKTD---------GSSLPSHVSHRAG 534

Qy          94 ILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVG 153
               |     |    |:| ||  | |  :| |  :      ::| | |     :   |   | |
Db         535 I-----LSFHKVSRSDSGNYTC--IASNSPQGEIRATVQLVVAVYVTFKLEPEPTTVYQG 587

Qy         154 KMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDD 213
                 |   || :|| | ||  |   | |   |:  || :   :      |:||   |  :|
Db         588 HTAMFQCQ-AEGDPVPHIQWKGKDKIL-DPSKLLPRIQIMPN------GSLVIYDVTTED 639

Qy         214 SGQYYCIASNDAG----------SARCEEQE----------MEVYDLNIGGIIGGVLV 251
               ||:| |||  |                || |          ::   |::|  :  :::
Db         640 SGKYTCIAGNSCNIKHREAFLYVVDKPAAEEDEGPSSHTPYKMIQTIGLSVGAAVAYIII 699

Qy         252 VLAVLALITLGICCAYRRGYFINNKQDGE 280
               || ::       |   |:   :   :||
Db         700 VLGLMF-----YCKKRRKAKRLKKHPEGE 723


Search completed: April 12, 2004, 09:15:14
Job time : 19 secs
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97369930; PubMed=9226371;
RA   Paoloni-Giacobino A., Chen H., Antonarakis S.E.;
RT   "Cloning of a novel human neural cell adhesion molecule gene (NCAM2)
RT   that maps to chromosome region 21q21 and is potentially involved in
RT   Down syndrome.";
RL   Genomics 43:43-51(1997).
RN   [2]
RP   CARBOHYDRATE-LINKAGE SITES ASN-445 AND ASN-562.
RX   MEDLINE=22660472; PubMed=12754519;
RA   Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT   "Identification and quantification of N-linked glycoproteins using
RT   hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL   Nat. Biotechnol. 21:660-666(2003).
CC   -!- FUNCTION: May play important roles in selective fasciculation and
CC       zone-to-zone projection of the primary olfactory axons.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed most strongly in adult and fetal
CC       brain.
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U75330; AAB80803.1; -.
DR   Genew; HGNC:7657; NCAM2.
DR   MIM; 602040; -.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0007158; P:neuronal cell adhesion; TAS.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW   Immunoglobulin domain; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    837       NEURAL CELL ADHESION MOLECULE 2.
FT   DOMAIN       20    697       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    698    718       POTENTIAL.
FT   DOMAIN      719    837       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       21    108       IG-LIKE C2-TYPE 1.
FT   DOMAIN      113    202       IG-LIKE C2-TYPE 2.
FT   DOMAIN      208    297       IG-LIKE C2-TYPE 3.
FT   DOMAIN      302    396       IG-LIKE C2-TYPE 4.
FT   DOMAIN      401    491       IG-LIKE C2-TYPE 5.
FT   DOMAIN      482    581       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      594    678       FIBRONECTIN TYPE-III 2.
FT   DISULFID     42     93       PROBABLE.
FT   DISULFID    136    186       PROBABLE.
FT   DISULFID    232    281       PROBABLE.
FT   DISULFID    322    380       PROBABLE.
FT   DISULFID    422    475       PROBABLE.
FT   CARBOHYD    177    177       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    219    219       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    309    309       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    406    406       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    419    419       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    445    445       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    474    474       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    562    562       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   837 AA;  92932 MW;  C3D034106C5741C1 CRC64;

  Query Match             10.1%;  Score 165;  DB 1;  Length 837;
  Best Local Similarity   24.3%;  Pred. No. 4.7e-06;
  Matches   72;  Conservative   31;  Mismatches  105;  Indels   88;  Gaps   15;

Qy         44 QEF---ESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSL 100
              |||   |  |: | :: |    | : |    :| ||    ||         |  :|   :|
Db        124 QEFKQGEDAEVVCRVSSSPA--PAVSWLYHNEEVTT--ISDN--------RLAMLANNNL 171

Qy        101 KIWNVTRRDSALYRCE--VVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPV------ 152
              :| |: : |  :||||  | || :            :  : : :  || |: :
Db        172 QILNINKSDEGIYRCEGRVEARGE-----------IDFRDIIVIVNVPPAISMPQKSFN 219

Qy        153 -----GKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFT 207
                  |:  |  |: | | | |  ||:||   :           |    |      |
Db        220 ATAERGEEMTFSCRAS-GSPEPAISWFRNGKLIE---------ENEKYILKGSNTELTVR 269

Qy        208 AVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAY 267
              :  | | | | |:| ||    | | : :          | |    :| |      |
Db        270 NIINSDGGPYVCRATNKAG-----EDEKQAF----------LQVFVQPHIIQLKNETTY 313

Qy        268 RRGYFINNKQDGESYKNPGKP----------DGVNYIRTDEEGDFR------HKSS 307
                | :   | |     |:|          || :   |:  | |      | ||
Db        314 ENGQ-VTLVCDAE-----GEPIPEITWKRAVDGFTFTEGDKSPDGRIEVKGQHGSS 363


RESULT 15
PTK7_CHICK
ID   PTK7_CHICK     STANDARD;      PRT;  1051 AA.
AC   Q91048;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Tyrosine-protein kinase-like 7 precursor (Kinase like protein).
GN   PTK7 OR KLG.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryonic brain;
RX   MEDLINE=91271300; PubMed=1711213;
RA   Chou Y.-H., Hayman M.J.;
RT   "Characterization of a member of the immunoglobulin gene superfamily
RT   that possibly represents an additional class of growth factor
RT   receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:4897-4901(1991).
CC   -!- FUNCTION: MAY FUNCTION AS A CELL ADHESION MOLECULE. LACKS PROBABLY
CC       THE CATALYTIC ACTIVITY OF TYROSINE KINASE.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN BONE MARROW, SPLEEN, BURSA,
CC       THYMUS AND BRAIN. WEAKLY EXPRESSED IN FIBROBLASTS. ALSO EXPRESSED
CC       IN EMBRYONIC LIVER.
CC   -!- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Insulin
CC       receptor subfamily.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M63437; AAA48933.1; -.
DR   PIR; A39712; A39712.
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OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS OF ARG-1178.
RX   MEDLINE=95204468; PubMed=7896816;
RA   Pulido R., Krueger N.X., Serra-Pages C., Saito H., Streuli M.;
RT   "Molecular characterization of the human transmembrane protein-
RT   tyrosine phosphatase delta. Evidence for tissue-specific expression of
RT   alternative human transmembrane protein-tyrosine phosphatase delta
RT   isoforms.";
RL   J. Biol. Chem. 270:6722-6728(1995).
RN   [2]
RP   SEQUENCE OF 390-1912 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=91006018; PubMed=2170109;
RA   Krueger N.X., Streuli M., Saito H.;
RT   "Structural diversity and evolution of human receptor-like protein
RT   tyrosine phosphatases.";
RL   EMBO J. 9:3241-3252(1990).
CC   -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC       tyrosine + phosphate.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=P23468-1; Sequence=Displayed;
CC       Name=2; Synonyms=Kidney;
CC         IsoId=P23468-2; Sequence=VSP_005147, VSP_005148, VSP_005149;
CC       Name=3; Synonyms=Fetal brain;
CC         IsoId=P23468-3; Sequence=VSP_005150;
CC   -!- PTM: A CLEAVAGE OCCURS THAT SEPARATES THE EXTRACELLULAR DOMAIN
CC       FROM THE TRANSMEMBRANE SEGMENT.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 8 fibronectin type III domains.
CC   -!- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L38929; AAC41749.1; -.
DR   EMBL; X54133; CAA38068.1; -.
DR   PIR; A56178; A56178.
DR   HSSP; P18052; 1YFO.
DR   Genew; HGNC:9668; PTPRD.
DR   MIM; 601598; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005001; F:transmembrane receptor protein tyrosine pho. . .; TAS.
DR   GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR   GO; GO:0007185; P:transmembrane receptor protein tyrosine pho. . .; TAS.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003962; FnIII_subd.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR000387; TYR_phosphatase.
DR   InterPro; IPR000242; Tyr_PP.
DR   Pfam; PF00041; fn3; 8.
DR   Pfam; PF00047; ig; 3.
DR   Pfam; PF00102; Y_phosphatase; 2.
DR   PRINTS; PR00014; FNTYPEIII.
DR   PRINTS; PR00700; PRTYPHPHTASE.
DR   SMART; SM00060; FN3; 8.
DR   SMART; SM00408; IGc2; 2.
DR   SMART; SM00194; PTPc; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
DR   PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR   PROSITE; PS50056; TYR_PHOSPHATASE_2; 2.
DR   PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 2.
KW   Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21   1912       PROTEIN-TYROSINE PHOSPHATASE DELTA.
FT   DOMAIN       21   1265       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   1266   1290       POTENTIAL.
FT   DOMAIN     1291   1912       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       24    114       IG-LIKE C2-TYPE 1.
FT   DOMAIN      126    224       IG-LIKE C2-TYPE 2.
FT   DOMAIN      236    318       IG-LIKE C2-TYPE 3.
FT   DOMAIN      320    414       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      417    513       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      516    606       FIBRONECTIN TYPE-III 3.
FT   DOMAIN      609    708       FIBRONECTIN TYPE-III 4.
FT   DOMAIN      711    822       FIBRONECTIN TYPE-III 5.
FT   DOMAIN      825    916       FIBRONECTIN TYPE-III 6.
FT   DOMAIN      918   1017       FIBRONECTIN TYPE-III 7.
FT   DOMAIN     1020   1137       FIBRONECTIN TYPE-III 8.
FT   DOMAIN     1375   1618       PROTEIN-TYROSINE PHOSPHATASE 1.
FT   DOMAIN     1619   1912       PROTEIN-TYROSINE PHOSPHATASE 2.
FT   ACT_SITE   1553   1553       PHOSPHOCYSTEINE INTERMEDIATE (BY
FT                                SIMILARITY).
FT   ACT_SITE   1844   1844       PHOSPHOCYSTEINE INTERMEDIATE (BY
FT                                SIMILARITY).
FT   SITE       1175   1178       CLEAVAGE (POTENTIAL).
FT   CARBOHYD    254    254       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    299    299       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    724    724       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    832    832       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    181    189       Missing (in isoform 2).
FT                                /FTId=VSP_005147.
FT   VARSPLIC    226    229       Missing (in isoform 2).
FT                                /FTId=VSP_005148.
FT   VARSPLIC    775    783       Missing (in isoform 2).
FT                                /FTId=VSP_005149.
FT   VARSPLIC    609   1137       Missing (in isoform 3).
FT                                /FTId=VSP_005150.
FT   MUTAGEN    1178   1178       R->A: 2.5-FOLD REDUCTION IN CLEAVAGE.
SQ   SEQUENCE   1912 AA;  214759 MW;  3AE8CBCD32182E26 CRC64;

  Query Match             10.4%;  Score 169.5;  DB 1;  Length 1912;
  Best Local Similarity   28.6%;  Pred. No. 5.6e-06;
  Matches   65;  Conservative   35;  Mismatches   76;  Indels   51;  Gaps   13;

Qy         39 RTPVVQEFESVELSCIITDSQTSDPR--IEW----KKIQDEQTTYVFFDNKIQGDLAGRA 92
              |||| |    |  ::  |  : | |||  | |    ||: :::   : ||:       |
Db         28 RTPVDQTGVSGGVASFICQA-TGDPRPKIVWNKKGKKVSNQRFEVIEFDD-------GSG 79

Qy         93 EILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPV 152
              :|   |:   | || |:| |  || |:  ||  :   ||| :     ::|:  |
Db         80 SVLRIQPLR----TPRDEAIYEC--VASNNVGEI-SVSTRLTVLRED-----QIPRGFPT 127

Qy        153 GKM------------ATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLNSE 200
               |             ||: |  | |:| |  :|::: :|: | |  | | :     | ||
Db        128 IDMGPQLKVVERTRTATMLCAAS-GNPDPEITWFKDFLPVDT-SNNNGRIK----QLRSE 181

Qy        201 T-------GTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              :       | |       : | |:| |:|:| ||:       : | :|
Db        182 SIGGTPIRGALQIEQSEESDQGKYECVATNSAGTRYSAPANLYVREL 228


RESULT 14
NCM2_HUMAN
ID   NCM2_HUMAN     STANDARD;      PRT;   837 AA.
AC   O15394;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 2 precursor (N-CAM 2).
GN   NCAM2 OR NCAM21.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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  Best Local Similarity   31.0%;  Pred. No. 2.8e-06;
  Matches   61;  Conservative   21;  Mismatches   69;  Indels   46;  Gaps    9;

Qy         47 ESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVT 106
              :|  | |:   |    | | | | :|   |          : :||  :|   ||:| :||
Db        233 QSAVLPCVA--SGLPAPVIRWMKNEDVLDT----------ESSGRLALLAGGSLEISDVT 280

Qy        107 RRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQES--- 163
              |:  | |  || |  | | |  ||||| |           : : | :: :||
Db        281 EDDAGTYFC--VADNGNKTI-EAQAELTVQVPPEF----------LKQPANIYARESMDI 327

Qy        164 ------EGHPRPHYSWYRN-DVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQ 216
                   | | |   | :| || :|:|     |:    |       |    : | | |
Db        328 VFECEVTGKPAPTVKWVKNGDVVIPSD-----YFKIVKEH------NLQVLGLVKSDEGF 376

Qy        217 YYCIASNDAGSARCEEQ 233
              | ||| || |:|:   |
Db        377 YQCIAENDVGNAQAGAQ 393


RESULT 12
NCA1_RAT
ID   NCA1_RAT       STANDARD;      PRT;   858 AA.
AC   P13596;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140)
DE   (NCAM-140).
GN   NCAM1 OR NCAM.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=88059265; PubMed=3680385;
RA   Small S.J., Shull G.E., Santoni M.-J., Akeson R.;
RT   "Identification of a cDNA clone that contains the complete coding
RT   sequence for a 140-kD rat NCAM polypeptide.";
RL   J. Cell Biol. 105:2335-2345(1987).
RN   [2]
RP   SEQUENCE OF 355-364 FROM N.A.
RX   MEDLINE=90166485; PubMed=2483093;
RA   Small S.J., Haines S.L., Akeson R.A.;
RT   "Polypeptide variation in an N-CAM extracellular immunoglobulin-like
RT   fold is developmentally regulated through alternative splicing.";
RL   Neuron 1:1007-1017(1988).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=1;
CC         Comment=A number of isoforms are produced;
CC       Name=1;
CC         IsoId=P13596-1; Sequence=Displayed;
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X06564; CAA29809.1; -.
DR   EMBL; M32611; AAA41679.1; -.
DR   PIR; S00846; IJRTNC.
DR   PDB; 1EPF; 27-OCT-00.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding;
KW   3D-structure.
FT   SIGNAL        1     19
FT   CHAIN        20    858       NEURAL CELL ADHESION MOLECULE 1, 140 kDa
FT                                 ISOFORM.
FT   DOMAIN       20    721       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    722    739       POTENTIAL.
FT   DOMAIN      740    858       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    111       IG-LIKE C2-TYPE 1.
FT   DOMAIN      116    205       IG-LIKE C2-TYPE 2.
FT   DOMAIN      212    302       IG-LIKE C2-TYPE 3.
FT   DOMAIN      309    414       IG-LIKE C2-TYPE 4.
FT   DOMAIN      417    502       IG-LIKE C2-TYPE 5.
FT   DOMAIN      514    615       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      616    712       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      152    156       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      161    165       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     96       BY SIMILARITY.
FT   DISULFID    139    189       BY SIMILARITY.
FT   DISULFID    235    288       BY SIMILARITY.
FT   DISULFID    330    396       BY SIMILARITY.
FT   DISULFID    437    490       BY SIMILARITY.
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    316    316       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    434    434       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    460    460       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    489    489       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   858 AA;  94658 MW;  EA1A06A4EA0550F6 CRC64;

  Query Match             10.4%;  Score 170.5;  DB 1;  Length 858;
  Best Local Similarity   26.3%;  Pred. No. 1.7e-06;
  Matches   61;  Conservative   41;  Mismatches   85;  Indels   45;  Gaps   12;

Qy         27 CLIGA---------VNLKSSNR-----TPVVQEPESVELSCIITDSQTS-DPRIEWKKIQ 71
              |:: |          ||:|   :       |  |||:  | : |: |  :|  | | ||
Db         96 CVVTAEDGTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                 :   |  :: |:  |  :|     |:|  : : |   ||||  ::||    ||:
Db        153 -----HKGRDVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |:: | | |      :  |      :|:  || | :::| | |  || ::  |:  :
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEE--- 258

Qy        188 PRFRNSSSHL-NSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
                :   |: : ::  |     | |:|  :| ||| | ||     ||:  ::
Db        259 ---EDDEKHIFSDDSSELTIRNVDKNDEAEYVCIAENKAG-----EQDASIH 302


RESULT 13
PTPD_HUMAN
ID   PTPD_HUMAN     STANDARD;      PRT;  1912 AA.
AC   P23468;
DT   01-NOV-1991 (Rel. 20, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Protein-tyrosine phosphatase delta precursor (EC 3.1.3.48) (R-PTP-
DE   delta).
GN   PTPRD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding.
FT   SIGNAL       1     19
FT   CHAIN       20   1115       NEURAL CELL ADHESION MOLECULE 1, 180 kDa
FT                                ISOFORM.
FT   DOMAIN      20    711       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   712    729       POTENTIAL.
FT   DOMAIN     730   1115       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      20    111       IG-LIKE C2-TYPE 1.
FT   DOMAIN     116    205       IG-LIKE C2-TYPE 2.
FT   DOMAIN     212    302       IG-LIKE C2-TYPE 3.
FT   DOMAIN     309    402       IG-LIKE C2-TYPE 4.
FT   DOMAIN     407    492       IG-LIKE C2-TYPE 5.
FT   DOMAIN     519    596       FIBRONECTIN TYPE-III 1.
FT   DOMAIN     625    692       FIBRONECTIN TYPE-III 2.
FT   DOMAIN     152    156       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN     161    165       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID    41     96       PROBABLE.
FT   DISULFID   139    189       PROBABLE.
FT   DISULFID   235    288       PROBABLE.
FT   DISULFID   330    386       PROBABLE.
FT   DISULFID   427    480       PROBABLE.
FT   CARBOHYD   222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   316    316       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   424    424       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   450    450       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   479    479       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC   810   1076       Missing (in isoform N-CAM 140).
FT                               /FTId=VSP_002588.
SQ   SEQUENCE   1115 AA;  119351 MW;  2C93DCD474CFBCAF CRC64;

  Query Match             10.5%;  Score 171.5;  DB 1;  Length 1115;
  Best Local Similarity   27.3%;  Pred. No. 1.9e-06;
  Matches   63;  Conservative   41;  Mismatches   84;  Indels   43;  Gaps   12;

Qy         27 CLIGA---------VNLKSSNR-----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ 71
              |:: |          ||:|   :       |  |||:  | : |: |  :|  | | ||
Db         96 CVVTAEDGTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                 :   |  :: |:  |  :|    |:|  : : |   ||||  ::||    ||:
Db        153 -----HKGRDVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
               |:: | | |      :  |     :|:  || | :::| | |  || ::  |:  :   :
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEE-D 260

Qy        188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
               | |:|     |::  :    | |:|  :| ||| | ||     ||:  ::
Db        261 ERSRSSV----SDSSEVTIRNVDKNDEAEYVCIAENKAG-----EQDASIH 302


RESULT 11
NEO1_RAT
ID   NEO1_RAT       STANDARD;      PRT;  1377 AA.
AC   P97603;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neogenin precursor (Fragment).
GN   NEO1 OR NGN.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97015074; PubMed=8861902;
RA   Keino-Masu K., Masu M., Hinck L., Leonardo E.D., Chan S.S.-Y.,
RA   Culotti J.G., Tessier-Lavigne M.;
RT   "Deleted in Colorectal Cancer (DCC) encodes a netrin receptor.";
RL   Cell 87:175-185(1996).
CC   -!- FUNCTION: May be involved as a regulatory protein in the
CC       transition of undifferentiated proliferating cells to their
CC       differentiated state. May also function as a cell adhesion
CC       molecule in a broad spectrum of embryonic and adult tissues.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily. DCC family.
CC   -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 6 fibronectin type III domains.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U68726; AAB41100.1; -.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003962; FnIII_subd.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 6.
DR   Pfam; PF00047; ig; 4.
DR   PRINTS; PR00014; FNTYPEIII.
DR   SMART; SM00060; FN3; 6.
DR   SMART; SM00408; IGc2; 3.
DR   PROSITE; PS50835; IG_LIKE; 4.
KW   Cell adhesion; Repeat; Signal; Transmembrane; Immunoglobulin domain;
KW   Glycoprotein.
FT   NON_TER      1      1
FT   SIGNAL      <1      2       POTENTIAL.
FT   CHAIN        3   1377       NEOGENIN.
FT   DOMAIN       3   1074       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM  1075   1095       POTENTIAL.
FT   DOMAIN    1096   1377       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      21    114       IG-LIKE C2-TYPE 1.
FT   DOMAIN     121    206       IG-LIKE C2-TYPE 2.
FT   DOMAIN     198    305       IG-LIKE C2-TYPE 3.
FT   DOMAIN     310    395       IG-LIKE C2-TYPE 4.
FT   DOMAIN     405    502       FIBRONECTIN TYPE-III 1.
FT   DOMAIN     505    598       FIBRONECTIN TYPE-III 2.
FT   DOMAIN     599    698       FIBRONECTIN TYPE-III 3.
FT   DOMAIN     704    798       FIBRONECTIN TYPE-III 4.
FT   DOMAIN     819    919       FIBRONECTIN TYPE-III 5.
FT   DOMAIN     920   1021       FIBRONECTIN TYPE-III 6.
FT   DOMAIN    1087   1090       POLY-VAL.
FT   DISULFID    43     98       BY SIMILARITY.
FT   DISULFID   142    190       BY SIMILARITY.
FT   DISULFID   239    289       BY SIMILARITY.
FT   DISULFID   331    379       BY SIMILARITY.
FT   CARBOHYD    42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   295    295       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   439    439       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   458    458       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   608    608       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   684    684       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   878    878       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1377 AA;  150637 MW;  E514ED8ABD1A63A9 CRC64;

  Query Match             10 5%;  Score 171;  DB 1;  Length 1377;
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FT   DOMAIN      212    302       IG-LIKE C2-TYPE 3.
FT   DOMAIN      309    402       IG-LIKE C2-TYPE 4.
FT   DOMAIN      407    492       IG-LIKE C2-TYPE 5.
FT   DOMAIN      519    596       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      625    692       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      152    156       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      161    165       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     96       PROBABLE.
FT   DISULFID    139    189       PROBABLE.
FT   DISULFID    235    288       PROBABLE.
FT   DISULFID    330    386       PROBABLE.
FT   DISULFID    427    480       PROBABLE.
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    316    316       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    348    348       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    424    424       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    450    450       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    479    479       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    261    268       ERSRSSVS -> DEKHIFSD (IN REF. 2).
FT   CONFLICT    273    273       V -> L (IN REF. 2).
FT   CONFLICT    354    355       QD -> KT (IN REF. 2).
FT   CONFLICT    549    549       T -> K (IN REF. 2).
FT   CONFLICT    572    572       T -> R (IN REF. 2).
FT   CONFLICT    575    575       D -> V (IN REF. 2).
FT   CONFLICT    589    594       MQPSES -> SAATEF (IN REF. 2).
FT   CONFLICT    600    602       PEL -> REP (IN REF. 2).
FT   CONFLICT    657    657       H -> D (IN REF. 2 AND 3).
SQ   SEQUENCE   725 AA;  80296 MW;  C2AEB8B4461C6B2F CRC64;

  Query Match          10.5%;  Score 171.5;  DB 1;  Length 725;
  Best Local Similarity   27.3%;  Pred. No. 1.1e-06;
  Matches   63;  Conservative   41;  Mismatches   84;  Indels   43;  Gaps   12;

Qy         27 CLIGA---------VNLKSSNR-----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ 71
              |:: |          ||:|   :      |  |||:  | : |: |  :|  | | ||
Db         96 CVVTAEDGTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                 :   |  :: |:  |  :|     |:|  : : |   ||||  ::||    ||:
Db        153 -----HKGRDVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |:: | | |      :  |      :|:  || | :::| | |  || ::  |:  :   :
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEE-D 260

Qy        188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
              | |:|     |::  :     | |:|  :| ||| | ||      ||:  ::
Db        261 ERSRSSV----SDSSEVTIRNVDKNDEAEYVCIAENKAG-----EQDASIH 302


RESULT 10
NCA1_MOUSE
ID   NCA1_MOUSE     STANDARD;      PRT;  1115 AA.
AC   P13595; Q61949;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM 180)
DE   (NCAM-180).
GN   NCAM1 OR NCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM N-CAM 180).
RC   STRAIN=C57BL/6;
RX   MEDLINE=87246524; PubMed=3595563;
RA   Barthels D., Santoni M.J., Wille W., Ruppert C., Chaix J.C.,
RA   Hirsch M.R., Fontecilla-Camps J.C., Goridis C.;
RT   "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
RT   a Mr 79,000 polypeptide without a membrane-spanning region.";
RL   EMBO J. 6:907-914(1987).
RN   [2]
RP   SEQUENCE OF 529-1115 FROM N.A. (ISOFORM N-CAM 140).
RC   STRAIN=C57BL/6;
RX   MEDLINE=88067687; PubMed=3684567;
RA   Santoni M.-J., Barthels D., Barbas J.A., Hirsch M.-R., Steinmetz M.,
RA   Goridis C., Wille W.;
RT   "Analysis of cDNA clones that code for the transmembrane forms of the
RT   mouse neural cell adhesion molecule (NCAM) and are generated by
RT   alternative RNA splicing.";
RL   Nucleic Acids Res. 15:8621-8641(1987).
RN   [3]
RP   SEQUENCE OF 642-1115 FROM N.A. (ISOFORM N-CAM 180).
RX   MEDLINE=88283628; PubMed=3396534;
RA   Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
RT   "Differential splicing and alternative polyadenylation generates
RT   distinct NCAM transcripts and proteins in the mouse.";
RL   EMBO J. 7:625-632(1988).
RN   [4]
RP   SEQUENCE OF 804-1081 FROM N.A. (ISOFORM N-CAM 180).
RC   STRAIN=C57BL/6J; TISSUE=Brain;
RX   MEDLINE=88247737; PubMed=2454455;
RA   Barthels D., Vopper G., Wille W.;
RT   "NCAM-180, the large isoform of the neural cell adhesion molecule of
RT   the mouse, is encoded by an alternatively spliced transcript.";
RL   Nucleic Acids Res. 16:4217-4225(1988).
RN   [5]
RP   SEQUENCE OF 702-1115 FROM N.A. (ISOFORM N-CAM 140).
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=89251563; PubMed=2721486;
RA   Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille M.;
RT   "Differential exon usage involving an unusual splicing mechanism
RT   generates at least eight types of NCAM cDNA in mouse brain.";
RL   EMBO J. 8:385-392(1989).
RN   [6]
RP   SEQUENCE OF 20-36.
RX   MEDLINE=86140120; PubMed=3512556;
RA   Rougon G., Marshak D.R.;
RT   "Structural and immunological characterization of the amino-terminal
RT   domain of mammalian neural cell adhesion molecules.";
RL   J. Biol. Chem. 261:3396-3401(1986).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=N-CAM 180;
CC         IsoId=P13595-1; Sequence=Displayed;
CC       Name=N-CAM 140;
CC         IsoId=P13595-2; Sequence=VSP_002588;
CC       Name=N-CAM 120;
CC         IsoId=P13594-1; Sequence=External;
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X07200; CAA30177.1; -.
DR   EMBL; Y00051; -; NOT_ANNOTATED_CDS.
DR   EMBL; X06328; CAA29641.1; -.
DR   EMBL; X07195; CAA30173.1; -.
DR   EMBL; X07244; CAA30230.1; -.
DR   EMBL; X15051; CAA33150.1; -.
DR   EMBL; X15052; CAA33151.1; -.
DR   PIR; A29673; IJMSNL.
DR   MGD; MGI:97281; Ncam1.
DR   InterPro; IPR008957; FN_III-like.
```

```
DR   SMART; SM00408; IGc2; 4.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing; Signal.
FT   SIGNAL        1     19       BY SIMILARITY.
FT   CHAIN        20   1092       NEURAL CELL ADHESION MOLECULE 2, 180 kDa
FT                              ISOFORM.
FT   DOMAIN       20    705       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    706    723       POTENTIAL.
FT   DOMAIN      724   1092       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    108       IG-LIKE C2-TYPE 1.
FT   DOMAIN      113    202       IG-LIKE C2-TYPE 2.
FT   DOMAIN      208    295       IG-LIKE C2-TYPE 3.
FT   DOMAIN      303    397       IG-LIKE C2-TYPE 4.
FT   DOMAIN      400    489       IG-LIKE C2-TYPE 5.
FT   DOMAIN      512    589       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      618    686       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      149    153       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      158    162       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     93       PROBABLE.
FT   DISULFID    136    186       PROBABLE.
FT   DISULFID    232    282       PROBABLE.
FT   DISULFID    323    379       PROBABLE.
FT   DISULFID    420    473       PROBABLE.
FT   CARBOHYD     82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    219    219       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    310    310       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    341    341       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    417    417       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    443    443       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    472    472       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   1092 AA;  118082 MW;  CD236EE0EF8B7AD1 CRC64;

  Query Match             10.8%;  Score 177;  DB 1;  Length 1092;
  Best Local Similarity   29.5%;  Pred. No. 6.5e-07;
  Matches   62;  Conservative   28;  Mismatches   86;  Indels   34;  Gaps   11;

Qy         30 GAVNLKSSNR-----TPVVQEFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN 82
              | ||||   :     |  |||   | : || |  :| |  | |: | :|     | |
Db        105 GTVNLKIYQKLTFKYAPTPQEFTEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159

Qy         83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEIVIELTVQVKPV 140
              :      |  :|    |:|  : : |   ||||  ::||    ||:   |:: | | |:
Db        160 DV------RFVVLANNYLQIRGIKKTDEGNYRCEGRILARG---EINYKDIQVIVNVPPL 210

Qy        141 TPV--CRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLN 198
                 ||     : :   | | :::| | |  || :   |:  |      |       |
Db        211 IQARQIRVNATANMDESVVLSC-DADGFPDPEISWLKKGEPI-EDGEEKISF-------N 261

Qy        199 SETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
              :   :    | |:|  :| |||:| || |
Db        262 EDKSEMTIYRVEKEDEAEYSCIANNQAGEA 291


RESULT 9
NCA2_MOUSE
ID   NCA2_MOUSE     STANDARD;      PRT;   725 AA.
AC   P13594; Q61950;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Neural cell adhesion molecule 1, 120 kDa isoform precursor (N-CAM 120)
DE   (NCAM-120).
GN   NCAM1 OR NCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=87246524; PubMed=3595563;
RA   Barthels D., Santoni M.-J., Wille W., Ruppert C., Caix J.-C.,
RA   Hirsch M.-R., Fontecilla-Camps J.-C., Goridis C.;
RT   "Isolation and nucleotide sequence of mouse NCAM cDNA that codes for
RT   a Mr 79,000 polypeptide without a membrane-spanning region.";
RL   EMBO J. 6:907-914(1987).
RN   [2]
RP   SEQUENCE OF 20-700 FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=89251563; PubMed=2721486;
RA   Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille M.;
RT   "Differential exon usage involving an unusual splicing mechanism
RT   generates at least eight types of NCAM cDNA in mouse brain.";
RL   EMBO J. 8:385-392(1989).
RN   [3]
RP   SEQUENCE OF 642-725 FROM N.A.
RX   MEDLINE=88283628; PubMed=3396534;
RA   Barbas J.A., Chaix J.C., Steinmetz M., Goridis C.;
RT   "Differential splicing and alternative polyadenylation generates
RT   distinct NCAM transcripts and proteins in the mouse.";
RL   EMBO J. 7:625-632(1988).
RN   [4]
RP   SEQUENCE OF 20-36.
RX   MEDLINE=86140120; PubMed=3512556;
RA   Rougon G., Marshak D.R.;
RT   "Structural and immunological characterization of the amino-terminal
RT   domain of mammalian neural cell adhesion molecules.";
RL   J. Biol. Chem. 261:3396-3401(1986).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=N-CAM 120;
CC         IsoId=P13594-1; Sequence=Displayed;
CC       Name=N-CAM 180;
CC         IsoId=P13595-1; Sequence=External;
CC       Name=N-CAM 140;
CC         IsoId=P13595-2; Sequence=External;
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y00051; CAA68263.1; -.
DR   EMBL; X15049; CAA33148.1; ALT_SEQ.
DR   EMBL; X07195; CAA30173.1; -.
DR   PIR; A29673; IJMSNG.
DR   PDB; 2NCM; 12-MAR-97.
DR   PDB; 3NCM; 23-JUL-99.
DR   MGD; MGI:97281; Ncam1.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Repeat; Alternative splicing;
KW   Immunoglobulin domain; Signal; Heparin-binding; GPI-anchor;
KW   3D-structure.
FT   SIGNAL        1     19
FT   CHAIN        20    725       NEURAL CELL ADHESION MOLECULE 1, 120 kDa
FT                              ISOFORM.
FT   DOMAIN       20    111       IG-LIKE C2-TYPE 1.
FT   DOMAIN      116    205       IG-LIKE C2-TYPE 2.
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RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley; TISSUE=Embryo;
RX   MEDLINE=22426066; PubMed=12537569;
RA   Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
RA   George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
RA   Rubin G.M., Celniker S.E.;
RT   "A Drosophila full-length cDNA resource.";
RL   Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC       (Potential).
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M23561; AAA28367.1; -.
DR   EMBL; AE001572; AAD19797.1; -.
DR   EMBL; AE003674; AAF54084.1; -.
DR   EMBL; AY051911; AAK93335.1; -.
DR   PIR; A31923; A31923.
DR   FlyBase; FBgn0000071; Ama.
DR   GO; GO:0005886; C:plasma membrane; IDA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Immunoglobulin domain; Glycoprotein; Membrane; GPI-anchor; Signal;
KW   Repeat.
FT   SIGNAL        1     23       POTENTIAL.
FT   CHAIN        24      ?       AMALGAM PROTEIN.
FT   PROPEP        ?    333       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN       25    128       IG-LIKE V-TYPE.
FT   DOMAIN      139    223       IG-LIKE C2-TYPE 1.
FT   DOMAIN      230    323       IG-LIKE C2-TYPE 2.
FT   DISULFID     46    117       PROBABLE.
FT   DISULFID    161    208       PROBABLE.
FT   DISULFID    251    307       PROBABLE.
FT   CARBOHYD     45     45       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    308    308       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     83     83       Q -> K (IN REF. 1).
SQ   SEQUENCE   333 AA;  36387 MW;  F644753DE3DB25F1 CRC64;
```

```
  Query Match           11.0%;  Score 180;  DB 1;  Length 333;
  Best Local Similarity  26.8%;  Pred. No. 8.2e-08;
  Matches   52;  Conservative   39;  Mismatches   83;  Indels   20;  Gaps    5;

Qy         35 KSSNRTPVVQEFESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEI 94
              ::: :: :| | :::||:|    :    | | | :           :   :    :
Db        143 ENTPKSTLVTEGQNLELTC--HANGFPKPTISWAR----------EHNAVMPAGGHL 187

Qy         95 LGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGK 154
              | : :|:| :| | |   | |  :|:|   : |: :| : |: :|   | |   | |
Db        188 LAEPTLRIRSVHRMDRGGYYC--IAQNGEGQPDKRLIRVEVEFRPQIAVQRPKIAQMVSH 245

Qy        155 MATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDS 214
              | | |   :|:| |   |::| |||   |  :    |::|   : | |   :| ::|
Db        246 SAELEC-SVQGYPAPTVVWHKNGVPL--QSSRHHEVANTASSSGTTTSVLRIDSVGEEDF 302

Qy        215 GQYYCIASNDAGSA 228
              | ||| |:|  | |
Db        303 GDYYCNATNKLGHA 316


RESULT 8
NCA2_XENLA
ID   NCA2_XENLA     STANDARD;      PRT;  1092 AA.
AC   P36335;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neural cell adhesion molecule 2, 180 kDa isoform precursor (N-CAM
DE   180).
GN   NCAM2.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93273239; PubMed=7684721;
RA   Tonissen K.F., Krieg P.A.;
RT   "Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus
RT   laevis are expressed during development and in adult tissues.";
RL   Gene 127:243-247(1993).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=1;
CC         Comment=A number of isoforms are produced;
CC       Name=1;
CC         IsoId=P36335-1; Sequence=Displayed;
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M76710; AAA49910.1; -.
DR   PIR; JN0635; JN0635.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
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RA   Krieg P.A., Sakaguchi D.S., Kintner C.R.;
RT   "Primary structure and developmental expression of a large
RT   cytoplasmic domain form of Xenopus laevis neural cell adhesion
RT   molecule (NCAM).";
RL   Nucleic Acids Res. 17:10321-10335(1989).
CC   -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC       neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC       neurites, etc.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=N-CAM 180;
CC         IsoId=P16170-1; Sequence=Displayed;
CC       Name=N-CAM 140;
CC         IsoId=P16170-2; Sequence=VSP_002589;
CC   -!- TISSUE SPECIFICITY: Expressed in neuron and in presumptive neural
CC       tissue.
CC   -!- DEVELOPMENTAL STAGE: THE MRNA ENCODING THIS LD-NCAM IS THE MAJOR
CC       TRANSCRIPT PRESENT IN BOTH MATERNAL RNA AND IN THE EMBRYO DURING
CC       EARLY NEURAL DEVELOPMENT.
CC   -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC   -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M25696; AAA49909.1; -.
DR   PIR; S09600; IJXLNL.
DR   HSSP; P56276; 1TLK.
DR   InterPro; IPR008957; FN_III-like.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 2.
DR   Pfam; PF00047; ig; 5.
DR   SMART; SM00060; FN3; 2.
DR   SMART; SM00408; IGc2; 5.
DR   PROSITE; PS50835; IG_LIKE; 5.
KW   Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW   Immunoglobulin domain; Alternative splicing; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20   1088       NEURAL CELL ADHESION MOLECULE 1, 180 kDa
FT                                ISOFORM.
FT   DOMAIN       20    705       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    706    723       POTENTIAL.
FT   DOMAIN      724   1088       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       20    108       IG-LIKE C2-TYPE 1.
FT   DOMAIN      113    202       IG-LIKE C2-TYPE 2.
FT   DOMAIN      209    294       IG-LIKE C2-TYPE 3.
FT   DOMAIN      303    397       IG-LIKE C2-TYPE 4.
FT   DOMAIN      400    484       IG-LIKE C2-TYPE 5.
FT   DOMAIN      512    589       FIBRONECTIN TYPE-III 1.
FT   DOMAIN      618    686       FIBRONECTIN TYPE-III 2.
FT   DOMAIN      149    153       HEPARIN-BINDING (POTENTIAL).
FT   DOMAIN      158    162       HEPARIN-BINDING (POTENTIAL).
FT   DISULFID     41     93       PROBABLE.
FT   DISULFID    136    186       PROBABLE.
FT   DISULFID    232    282       PROBABLE.
FT   DISULFID    323    379       PROBABLE.
FT   DISULFID    420    473       PROBABLE.
FT   CARBOHYD     82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    219    219       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    310    310       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    341    341       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    417    417       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    443    443       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    472    472       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    804   1049       Missing (in isoform N-CAM 140).
FT                                /FTId=VSP_002589.
SQ   SEQUENCE   1088 AA;  117778 MW;  62738B55B03F3E83 CRC64;

  Query Match           11.4%;  Score 186;  DB 1;  Length 1088;
  Best Local Similarity   29.9%;  Pred. No. 1.1e-07;
  Matches   63;  Conservative   30;  Mismatches   82;  Indels   36;  Gaps   12;

Qy         30 GAVNLK-----SSNRTPVVQEFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN 82
              |  ||||     :     |  |||:  | : || |  :| |   | |: | :|      | |
Db        105 GTVNLKIYQKLTFKNAPTPQEFKEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159

Qy         83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARND--RKEIDEIV-IELTVQV 137
               :      |  :|    |:|  : : |   ||||  ::|| :   |:|  || :  |:|
Db        160 DV------RFVVLANNYLQIRGIKKTDEGTYRCEGRILARGEINYKDIQVIVNVPPTIQA 213

Qy        138 KPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHL 197
              : :    ||      : :   | | :::| | |  || :   |:  |       |
Db        214 RQL----RVNATANMAESVVLSC-DADGFPDPEISWLKKGEPI-EDGEEKISF------- 260

Qy        198 NSETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
              | :   :    | |||  :| |||:| || |
Db        261 NEDQSEMTIHHVEKDDEAEYSCIANNQAGEA 291


RESULT 7
AMAL_DROME
ID   AMAL_DROME     STANDARD;      PRT;   333 AA.
AC   P15364; Q9V3A5;
DT   01-APR-1990 (Rel. 14, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Amalgam protein precursor.
GN   AMA OR BG:DS00276.6 OR CG2198.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Oregon-R;
RX   MEDLINE=89028670; PubMed=3141062;
RA   Seeger M.A., Haffley L., Kaufman T.C.;
RT   "Characterization of amalgam: a member of the immunoglobulin
RT   superfamily from Drosophila.";
RL   Cell 55:589-600(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RA   Celniker S.E., Pfeiffer B.D., Knafels J., Martin C.H., Mayeda C.A.,
RA   Palazzolo M.J.;
RT   "Complete sequence of the Antennapedia complex of Drosophila.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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Db          66 GDIRGLVCYNNKITASYENRV-TFSDTGITFHSVTRKDTGMYTC-MVSDEGGNTYGEVTV 123

Qy         132 ELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFR 191

Db         124 QLIVLVPPSKPTINVPSSVTIGTRAVLTCSERDGSPPSEYKWFKDGVEMPLEPKSNRAFS 183

Qy         192 NSSSHLNSETGTLVFTAVHKDDSGQYYCIASND-AGSARCEEQEMEVYDLNIGGIIGGVL 250

Db         184 NSSYTLNQKTGELIFDPVSASDTGDFTCQAQNGYASPVKSDTVHMDAVELNVGGIVAAVF 243

Qy         251 VVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTD--EEGDFRHKSSF 308

Db         244 VTLILLGALIFGIWFAYSRGYFDRAKK-GTSNKK------VIYSQPNARSDGEFRQTSSF 296

Qy         309 VI 310

Db         297 LV 298


RESULT 5
A33_HUMAN
ID   A33_HUMAN      STANDARD;      PRT;   319 AA.
AC   Q99795;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Cell surface A33 antigen precursor (Glycoprotein A33).
GN   GPA33.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   TISSUE=Colon carcinoma;
RX   MEDLINE=97165045; PubMed=9012807;
RA   Heath J.K., White S.J., Johnstone C.N., Catimel B., Simpson R.J.,
RA   Moritz R.L., Tu G.-F., Ji H., Whitehead R.H., Groenen L.C.,
RA   Scott A.M., Ritter G., Cohen L., Welt S., Old L.J., Nice E.C.,
RA   Burgess A.W.;
RT   "The human A33 antigen is a transmembrane glycoprotein and a novel
RT   member of the immunoglobulin superfamily.";
RL   Proc. Natl. Acad. Sci. U.S.A. 94:469-474(1997).
RN   [2]
RP   POST-TRANSLATIONAL MODIFICATIONS.
RX   MEDLINE=97396159; PubMed=9245713;
RA   Ritter G., Cohen L.S., Nice E.C., Catimel B., Burgess A.W.,
RA   Moritz R.L., Ji H., Heath J.K., White S.J., Welt S., Old L.J.,
RA   Simpson R.J.;
RT   "Characterization of posttranslational modifications of human A33
RT   antigen, a novel palmitoylated surface glycoprotein of human
RT   gastrointestinal epithelium.";
RL   Biochem. Biophys. Res. Commun. 236:682-686(1997).
CC   -!- FUNCTION: May play a role in cell-cell recognition and signaling.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in normal gastrointestinal
CC       epithelium and in 95% of colon cancers.
CC   -!- PTM: N-GLYCOSYLATED, CONTAINS APPROXIMATELY 8 KDA OF N-LINKED
CC       CARBOHYDRATE.
CC   -!- PTM: Palmitoylated.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U79725; AAC50957.1; -.
DR   Genew; HGNC:4445; GPA33.
DR   MIM; 602171; -.
DR   GO; GO:0005888; C:proteoglycan integral to plasma membrane; TAS.
DR   GO; GO:0004872; F:receptor activity; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; Lipoprotein; Palmitate; Glycoprotein;
KW   Transmembrane; Signal; Antigen.
FT   SIGNAL        1     21
FT   CHAIN        22    319       CELL SURFACE A33 ANTIGEN.
FT   DOMAIN       22    235       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    236    256       POTENTIAL.
FT   DOMAIN      257    319       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       22    134       IG-LIKE V-TYPE.
FT   DOMAIN      140    227       IG-LIKE C2-TYPE.
FT   DOMAIN      258    261       POLY-CYS.
FT   DISULFID     43    117       POTENTIAL.
FT   DISULFID    146    222       POTENTIAL.
FT   DISULFID    162    211       POTENTIAL.
FT   CARBOHYD    112    112       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    200    200       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   319 AA;  35632 MW;  9BFC7AAF45C2408E CRC64;

  Query Match             14.2%;  Score 231.5;  DB 1;  Length 319;
  Best Local Similarity   26.8%;  Pred. No. 3.7e-12;
  Matches   81;  Conservative   46;  Mismatches  134;  Indels   41;  Gaps   13;

Qy          29 IGAVNLKSSNRTPVVQEFESVELSCII-TDSQTSDPRIEWKKIQDEQTTYVF---FDNK- 83

Db          19 VDAISVETPQDVLRASQGKSVTLPCTYHTSTSSREGLIQWDKLLLTHTERVVIWPFSNKN 78

Qy          84 -IQGDL-------AGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTV 135

Db          79 YIHGELYKNRVSISNNAE-QSDASITIDQLTMADNGTYECSVSLMSDLEGNTKSRVRLLV 137

Qy         136 QVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSS 195

Db         138 LVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEQPLAQPASGQPVS 197

Qy         196 HLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCE-EQEMEVYDLNIG---GIIGGVLV 251

Db         198 LKNIST----------DTSGYYICTSSNEEGTQFCNITVAVRSPSMNVALYVGIAVGVVA 247

Qy         252 VLAVLALITLGICCAYRRGYFIN--NKQDG----ESYKNPGKPDGVNYI--RTDEEGDFR 303

Db         248 ALIIIGIIIYCCCC---RGKDDNTEDKEDARPNREAYEEP--PEQLRELSRERFEEDDYR 302

Qy         304 HK 305

Db         303 QE 304


RESULT 6
NCA1_XENLA
ID   NCA1_XENLA     STANDARD;      PRT;  1088 AA.
AC   P16170;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-APR-1990 (Rel. 14, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Neural cell adhesion molecule 1, 180 kDa isoform precursor (N-CAM
DE   180).
GN   NCAM1.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS N-CAM 140 AND N-CAM 180).
RX   MEDLINE=90098871; PubMed=2481269;
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CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF111713; AAD42050.1; -.
DR   EMBL; AF207907; AAF22829.1; -.
DR   EMBL; AF172398; AAD48877.1; -.
DR   EMBL; AL136649; CAB66584.1; -.
DR   EMBL; AY358896; AAQ89255.1; -.
DR   EMBL; BC001533; AAH01533.1; -.
DR   PIR; A59406; S56749.
DR   Genew; HGNC:14685; F11R.
DR   MIM; 605721; -.
DR   GO; GO:0005911; C:intercellular junction; TAS.
DR   GO; GO:0006954; P:inflammatory response; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal.
FT   SIGNAL       1     25       POTENTIAL.
FT   CHAIN       26    299       JUNCTIONAL ADHESION MOLECULE 1.
FT   DOMAIN      26    238       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   239    259       POTENTIAL.
FT   DOMAIN     260    299       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      27    125       IG-LIKE V-TYPE 1.
FT   DOMAIN     135    228       IG-LIKE V-TYPE 2.
FT   DISULFID    50    109       POTENTIAL.
FT   DISULFID   153    212       POTENTIAL.
FT   CARBOHYD   185    185       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   299 AA;  32583 MW;  D95DE2FEA23D2851 CRC64;

  Query Match             25.6%;  Score 419;  DB 1;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 6e-28;
  Matches  101;  Conservative   47;  Mismatches  138;  Indels   22;  Gaps    7;

Qy          8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
              |  ||     | | :|     :|:| : ||     : |   |:|||    |  | ||:||
Db          9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              |  | :  |  | ::|||       |   |  |  :   :||| |:  |  | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
             |: ::| | |  |   :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
               | |||  ||  || |||  :   |:|:| | | |  |:         ||  : |:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
              ||| | :| ::  ||  || ||:|    |:   |    |  |              ||:|
Db        241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy        303 RHKSSFVI 310
              :  |||::
Db        292 KQTSSFLV 299


RESULT 4
JAM1_BOVIN
ID   JAM1_BOVIN     STANDARD;      PRT;   298 AA.
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AC   Q9XT56;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Junctional adhesion molecule 1 precursor (JAM).
GN   F11R OR JAM1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99323940; PubMed=10395639;
RA   Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA   Iwamatsu A., Kita T.;
RT   "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RT   of junctional adhesion molecule in human endothelial cells.";
RL   J. Immunol. 163:553-557(1999).
CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC       formation. Appears early in primordial forms of cell junctions and
CC       recruits PARD3. The association of the PARD6-PARD3 complex may
CC       prevent the interaction of PARD3 with JAM1, thereby preventing
CC       tight junction assembly (By similarity). Plays a role in
CC       regulating monocyte transmigration involved in integrity of
CC       epithelial barrier. Involved in platelet activation.
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC       association between PARD3 and PARD6B probably disrupts this
CC       interaction (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC       epithelial and endothelial cells.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF111714; AAD42051.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal.
FT   SIGNAL       1     24       POTENTIAL.
FT   CHAIN       25    298       JUNCTIONAL ADHESION MOLECULE 1.
FT   DOMAIN      25    237       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   238    258       POTENTIAL.
FT   DOMAIN     259    298       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      28    124       IG-LIKE V-TYPE 1.
FT   DOMAIN     134    227       IG-LIKE V-TYPE 2.
FT   DISULFID    49    108       POTENTIAL.
FT   DISULFID   152    211       POTENTIAL.
FT   CARBOHYD   184    184       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   298 AA;  32456 MW;  714FE1C1714769A2 CRC64;

  Query Match             24.7%;  Score 403.5;  DB 1;  Length 298;
  Best Local Similarity   33.8%;  Pred. No. 1.2e-26;
  Matches  102;  Conservative   48;  Mismatches  125;  Indels   27;  Gaps   10;

Qy         21 LLLFRGCLI-------GAVNLKSSNRTPVVQ--EFESVELSCIITDSQTSDPRIEWKKIQ 71
              ||||   ::      |||       |||:  |    :|||  : |  | ||:|||
Db         12 LLLFTSMILCSLALGRGAV----QTYEPVVRVPENNPAKLSC--SYSGFSSPRVEWKFTH 65

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVI 131
              :    | ::|||       |       | :   :|||:|: :| | :|:        |: :
```

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DR   GO; GO:0005515; F:protein binding; IPI.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00406; IGv; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Tight junction; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW   Repeat; Signal; 3D-structure.
FT   SIGNAL        1     26       POTENTIAL.
FT   CHAIN        27    300       JUNCTIONAL ADHESION MOLECULE 1.
FT   DOMAIN       27    238       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    239    259       POTENTIAL.
FT   DOMAIN      260    299       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       28    122       IG-LIKE V-TYPE 1.
FT   DOMAIN      134    230       IG-LIKE V-TYPE 2.
FT   DISULFID     49    108       POTENTIAL.
FT   DISULFID    152    212       POTENTIAL.
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    185    185       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   300 AA;  32368 MW;  391F3E48FF3B97EC CRC64;

  Query Match           27.5%;  Score 449.5;  DB 1;  Length 300;
  Best Local Similarity  35.2%;  Pred. No. 1.7e-30;
  Matches  105;  Conservative   56;  Mismatches  122;  Indels   15;  Gaps    7;

Qy         20 LLLLFRGCLIGAV-----NLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEWKKIQDEQ 74
              || ||   ::|::     :: ::     | | ||::|:|  | |  | ||:||| :|
Db         11 LLFLFTSMILGSLVQGKGSVYTAQSDVQVPENESIKLTC--TYSGFSSPRVEWKFVQGST 68

Qy         75 TTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELT 134
              | | ::::|   | |     :  :  :|||:|:  | | :|:   :   |: | ||
Db         69 TALVCYNSQITAPYADRV-TFSSSGITFSSVTRKDNGEYTC-MVSEEGGQNYGEVSIHLT 126

Qy        135 VQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT-DSRANPRFRNS 193
              | | |   |   || :| :|  | | | | :| |   |||::: : : | |::    | ||
Db        127 VLVPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNS 186

Qy        194 SSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSA-RCEEQEMEVYDLNIGGIIGGVLVV 252
              |  :: ::| |:|  |   |||:||| | |  |:| | |   |:  :||:|||:  |||
Db        187 SFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGIVAAVLVT 246

Qy        253 LAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
              | :| |:  |:  || ||||   |:       |||    :   |  ||:|:  |||::
Db        247 LILLGLLIFGVWFAYSRGYFETTKKG----TAPGKKVIYSQPSTRSEGEFKQTSSFLV 300


RESULT 3
JAM1_HUMAN
ID   JAM1_HUMAN     STANDARD;      PRT;   299 AA.
AC   Q9Y624;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Junctional adhesion molecule 1 precursor (JAM) (Platelet adhesion
DE   molecule 1) (PAM-1) (Platelet F11 receptor) (UNQ264/PRO301).
GN   F11R OR JAM1 OR JCAM.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99323940; PubMed=10395639;
RA   Ozaki H., Ishii K., Horiuchi H., Arai H., Kawamoto T., Okawa K.,
RA   Iwamatsu A., Kita T.;
RT   "Combined treatment of TNF-alpha and IFN-gamma causes redistribution
RT   of junctional adhesion molecule in human endothelial cells.";
RL   J. Immunol. 163:553-557(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Sobocka M.B., Sobocki T., Rushbrook J.I., Banerjee P., Weiss C.,
RA   Kornecki E.;
RT   "Molecular cloning and sequencing of the cDNA of F11 receptor, a
RT   novel Ig superfamily member from human platelets.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Naik U.P., Naik M.U., DeLeon P., Spychala J.;
RT   "Cloning and characterization of PAM-1, a novel platelet adhesion
RT   molecule involved in platelet activation.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=21154917; PubMed=11230166;
RA   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA   Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
RA   Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA   Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA   Wambutt R., Korn B., Klein M., Poustka A.;
RT   "Towards a catalog of human genes and proteins: sequencing and
RT   analysis of 500 novel complete protein coding human cDNAs.";
RL   Genome Res. 11:422-435(2001).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22887296; PubMed=12975309;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC       formation. Appears early in primordial forms of cell junctions and
CC       recruits PARD3. The association of the PARD6-PARD3 complex may
CC       prevent the interaction of PARD3 with JAM1, thereby preventing
CC       tight junction assembly (By similarity). Plays a role in
CC       regulating monocyte transmigration involved in integrity of
CC       epithelial barrier. Involved in platelet activation.
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC       association between PARD3 and PARD6B probably disrupts this
CC       interaction (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC       epithelial and endothelial cells.
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CC   -!- FUNCTION: MAY PLAY A ROLE IN THE PROCESSES OF LYMPHOCYTE HOMING TO
CC       SECONDARY LYMPHOID ORGANS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: PROMINENTLY EXPRESSED ON HIGH ENDOTHELIAL
CC       VENULES BUT IS ALSO PRESENT ON THE ENDOTHELIA OF OTHER VESSELS.
CC       LOCALIZED TO THE INTERCELLULAR BOUNDARIES OF HIGH ENDOTHELIAL
CC       CELLS.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC   -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC   -!- DATABASE: NAME=PROW; NOTE=PROW 2:1-3(2001);
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/guide/1652492186_g.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF255910; AAF81223.1; -.
DR   EMBL; AY016009; AAG49022.1; -.
DR   EMBL; BC017779; AAH17779.1; -.
DR   Genew; HGNC:14686; JAM2.
DR   MIM; 606870; -.
DR   GO; GO:0005887; C:integral to plasma membrane; NAS.
DR   GO; GO:0016337; P:cell-cell adhesion; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; Glycoprotein; Transmembrane; Signal.
FT   SIGNAL        1     20       POTENTIAL.
FT   CHAIN        21    298       JUNCTIONAL ADHESION MOLECULE 2.
FT   DOMAIN       21    238       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    239    259       POTENTIAL.
FT   DOMAIN      260    298       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       32    127       IG-LIKE V-TYPE.
FT   DOMAIN      134    238       IG-LIKE C2-TYPE.
FT   DISULFID     50    109       POTENTIAL.
FT   DISULFID    155    214       POTENTIAL.
FT   CARBOHYD     98     98       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    187    187       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    236    236       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   298 AA;  33207 MW;  CA78E518E22DCAEE CRC64;

  Query Match           29.5%;  Score 483;  DB 1;  Length 298;
  Best Local Similarity  36.2%;  Pred. No. 2.5e-33;
  Matches  115;  Conservative   59;  Mismatches  116;  Indels   28;  Gaps   10;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIG-----AVNLKSSNRTPVVQ--EFESVELSC 53
              || |   ||           |||| |  ::      |    :      ||   |::   |:|
Db          1 MARRSRHRL----------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC 50

Qy         54 IITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALY 113
                |  :|   |:||||:     ::|::   :|||   |||::   :::| |||| |:  |
Db         51 -KTPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107

Qy        114 RCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
              |||| | ::: : ::|  : | | | |  | | || :   | :  | |||: ||:| | |:
Db        108 RCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

Qy        173 WYRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
              |::: : |  : |   :  |||  :|::|||| |  | | |:|:| | | | |  | ||
Db        168 WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227

Qy        233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVN 292
              : |:| |||| |||  |:|| |::  ||:| | |:|||  :|:   |::   | :  :
Db        228 KRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF--SKE--TSFQ---KSNSSS 280

Qy        293 YIRTDEEGDFRHKSSFVI 310
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                |  | ||:|  ||:|
Db        281 KATTMSENDFKHTKSFII 298

RESULT 2
JAM1_MOUSE
ID   JAM1_MOUSE     STANDARD;      PRT;   300 AA.
AC   O88792;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Junctional adhesion molecule 1 precursor (JAM).
GN   F11R OR JAM1 OR JCAM1 OR JCAM.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98327120; PubMed=9660867;
RA   Martin-Padura I., Lostaglio S., Schneemann M., Williams L., Romano M.,
RA   Fruscella P., Panzeri C., Stoppacciaro A., Ruco L., Villa A.,
RA   Simmons D., Dejana E.;
RT   "Junctional adhesion molecule, a novel member of the immunoglobulin
RT   superfamily that distributes at intercellular junctions and modulates
RT   monocyte transmigration.";
RL   J. Cell Biol. 142:117-127(1998).
RN   [2]
RP   INTERACTION WITH PARD3.
RX   MEDLINE=21340266; PubMed=11447115;
RA   Ebnet K., Suzuki A., Horikoshi Y., Hirose T.,
RA   Meyer zu Brickwedde M.-K., Ohno S., Vestweber D.;
RT   "The cell polarity protein ASIP/PAR-3 directly associates with
RT   junctional adhesion molecule (JAM).";
RL   EMBO J. 20:3738-3748(2001).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 212-238.
RX   MEDLINE=21391702; PubMed=11500366;
RA   Kostrewa D., Brockhaus M., D'Arcy A., Dale G.E., Nelboeck P.,
RA   Schmid G., Mueller F., Bazzoni G., Dejana E., Bartfai T.,
RA   Winkler F.K., Hennig M.;
RT   "X-ray structure of junctional adhesion molecule: structural basis for
RT   homophilic adhesion via a novel dimerization motif.";
RL   EMBO J. 20:4391-4398(2001).
CC   -!- FUNCTION: Seems to plays a role in epithelial tight junction
CC       formation. Appears early in primordial forms of cell junctions and
CC       recruits PARD3. The association of the PARD6-PARD3 complex may
CC       prevent the interaction of PARD3 with JAM1, thereby preventing
CC       tight junction assembly. Plays a role in regulating monocyte
CC       transmigration involved in integrity of epithelial barrier.
CC       Involved in platelet activation.
CC   -!- SUBUNIT: Interacts with the first PDZ domain of PARD3. The
CC       association between PARD3 and PARD6B probably disrupts this
CC       interaction.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC       Localized at tight junctions of both epithelial and endothelial
CC       cells.
CC   -!- TISSUE SPECIFICITY: Localized at tight junctions of both
CC       epithelial and endothelial cells.
CC   -!- SIMILARITY: Belongs to the immunoglobulin superfamily.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U89915; AAC32982.1; -.
DR   PDB; 1F97; 22-AUG-01.
DR   MGD; MGI:1321398; F11r.
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:08:53 ; Search time 17 Seconds
(without alignments)
949.515 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 1635
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	483	29.5	298	1	JAM2_HUMAN	P57087 homo sapien
2	449.5	27.5	300	1	JAM1_MOUSE	O88792 mus musculu
3	419	25.6	299	1	JAM1_HUMAN	Q9y624 homo sapien
4	403.5	24.7	298	1	JAM1_BOVIN	Q9xt56 bos taurus
5	231.5	14.2	319	1	A33_HUMAN	Q99795 homo sapien
6	186	11.4	1088	1	NCA1_XENLA	P16170 xenopus lae
7	180	11.0	333	1	AMAL_DROME	P15364 drosophila
8	177	10.8	1092	1	NCA2_XENLA	P36335 xenopus lae
9	171.5	10.5	725	1	NCA2_MOUSE	P13594 mus musculu
10	171.5	10.5	1115	1	NCA1_MOUSE	P13595 mus musculu
11	171	10.5	1377	1	NEO1_RAT	P97603 rattus norv
12	170.5	10.4	858	1	NCA1_RAT	P13596 rattus norv
13	169.5	10.4	1912	1	PTPD_HUMAN	P23468 homo sapien
14	165	10.1	837	1	NCM2_HUMAN	O15394 homo sapien
15	164.5	10.1	1051	1	PTK7_CHICK	Q91048 gallus gall
16	164.5	10.1	3707	1	PGBM_MOUSE	Q05793 mus musculu
17	164	10.0	837	1	NCM2_MOUSE	O35136 mus musculu
18	163.5	10.0	853	1	NCA1_BOVIN	P31836 bos taurus
19	163	10.0	1493	1	NEO1_MOUSE	P97798 mus musculu
20	162.5	9.9	6632	1	UN89_CAEEL	O01761 caenorhabdi
21	161.5	9.9	365	1	CXAR_HUMAN	P78310 homo sapien
22	158	9.7	1091	1	NCA1_CHICK	P13590 gallus gall
23	155.5	9.5	761	1	NCA2_HUMAN	P13592 homo sapien
24	155.5	9.5	848	1	NCA1_HUMAN	P13591 homo sapien
25	155.5	9.5	1284	1	NRCA_CHICK	P35331 gallus gall
26	153.5	9.4	1461	1	NEO1_HUMAN	Q92859 homo sapien
27	153	9.4	344	1	NTRI_HUMAN	Q9p121 homo sapien
28	151.5	9.3	349	1	LACH_SCHAM	Q26474 schistocerc
29	151	9.2	353	1	CEPU_CHICK	Q90773 gallus gall
30	150.5	9.2	702	1	CEA5_HUMAN	P06731 homo sapien
31	149.5	9.1	1897	1	PTPF_HUMAN	P10586 homo sapien
32	149	9.1	338	1	LAMP_CHICK	Q98919 gallus gall
33	148.5	9.1	338	1	LAMP_RAT	Q62813 rattus norv
34	148.5	9.1	646	1	MU18_HUMAN	P43121 homo sapien
35	148	9.1	344	1	NTRI_MOUSE	Q99pj0 mus musculu
36	147	9.0	344	1	NTRI_RAT	Q62718 rattus norv
37	146.5	9.0	338	1	LAMP_HUMAN	Q13449 homo sapien
38	146	8.9	365	1	CXAR_MOUSE	P97792 mus musculu
39	145.5	8.9	345	1	OPCM_RAT	P32736 rattus norv
40	145.5	8.9	4391	1	PGBM_HUMAN	P98160 homo sapien
41	145	8.9	521	1	CEA1_MOUSE	P31809 mus musculu
42	144	8.8	847	1	CD22_HUMAN	P20273 homo sapien
43	143.5	8.8	1277	1	CAML_FUGRU	Q98902 fugu rubrip
44	143.5	8.8	1443	1	NEO1_CHICK	Q90610 gallus gall
45	141	8.6	345	1	OPCM_BOVIN	P11834 bos taurus

ALIGNMENTS

RESULT 1
JAM2_HUMAN
ID JAM2_HUMAN STANDARD; PRT; 298 AA.
AC P57087;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Junctional adhesion molecule 2 precursor (Vascular endothelial
DE junction-associated molecule) (VE-JAM).
GN JAM2 OR VEJAM OR C21ORF43.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vascular endothelial cells;
RX MEDLINE=20317114; PubMed=10779521;
RA Palmeri D., van Zante A., Huang C.C., Hemmerich S., Rosen S.D.;
RT "Vascular endothelial junction-associated molecule, a novel member of
RT the immunoglobulin superfamily, is localized to intercellular
RT boundaries of endothelial cells.";
RL J. Biol. Chem. 275:19139-19145(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20507930; PubMed=10945976;
RA Cunningham S.A., Arrate M.P., Rodriguez J.M., Bjercke R.J.,
RA Vanderslice P., Morris A.P., Brock T.A.;
RT "A novel protein with homology to the junctional adhesion molecule:
RT Characterization of leukocyte interactions.";
RL J. Biol. Chem. 275:34750-34756(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

```
  Best Local Similarity   27.0%;  Pred. No. 8.1e-05;
  Matches   63;  Conservative   35;  Mismatches   74;  Indels   61;  Gaps   13;

Qy          1 MALRRPPRLRLCARLPDFPLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ::: || : :   ||:           | |:|          : : | || :
Db       2428 LSVHGPPTVSV---LPE-----------GPVHVKMG---------KDITLECISSGEPR 2463

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              | ||  |       | :    |::  : |        ||| :|    |:  | |:  |:
Db       2464 SSPR--W--------TRLGIPVKLEPRMFGLMN--SHAMLKIASVKPSDAGTYVCQ--AQ 2509

Qy        121 N----DRKEIDEIVIELTVQVKPVTPVCRVPKA---VPVGKMATLHCQESEGHPRPHYSW 173
              |     :|:: |:::: |  | | ||  :| ::   :  |  ||||| : |:| |  |
Db       2510 NALGTAQKQV-ELIVD-TGTVAPGTPQVQVEESELTLEAGHTATLHC-SATGNPPPTIHW 2566

Qy        174 YRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAG 226
              :   |||   |              | |||   | : ||||| | |:| ||
Db       2567 SKLRAPLPWQHRI------------EGNTLVIPRVAQQDSGQYICNATNSAG 2606


RESULT 14
IJBONC
neural cell adhesion molecule short domain form precursor - bovine
N;Alternate names: NCAM-140
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: A32976; A38778; B44290; S05402
R;Lipkin, V.M.; Khramtsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Raki
FEBS Lett. 254, 69-73, 1989
A;Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence and
A;Reference number: A32976; MUID:89378239; PMID:2776887
A;Accession: A32976
A;Molecule type: mRNA
A;Residues: 1-853 <LIP>
A;Cross-references: GB:X16451; NID:g60; PIDN:CAA34470.1; PID:g61
A;Accession: A38778
A;Molecule type: protein
A;Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-562;
A;Note: the authors identified this protein as calmodulin-independent adenylate cyclase
R;Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of m
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: B44290
A;Molecule type: protein
A;Residues: 20-36 <ROU>
A;Note: 23-Glu was also found
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Various forms of NCAM are produced by alternative splicing.
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-853/Product: neural cell adhesion molecule, short domain form #status experimental
F;20-719/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-288/Domain: immunoglobulin homology <IMM3>
F;261-270/Region: NCAM binding #status predicted
F;321-396/Domain: immunoglobulin homology <IMM4>
F;428-490/Domain: immunoglobulin homology <IMM5>
F;527-604/Domain: fibronectin type III repeat homology <FN3A>
F;633-693/Domain: fibronectin type III repeat homology <FN3B>
F;720-737/Domain: transmembrane #status predicted <TMM>
F;738-853/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-286,328-394,435-488/Disulfide bonds: #status predicted
F;222,314,346,432,458,487/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             10.0%;  Score 163.5;  DB 1;  Length 853;
  Best Local Similarity   27.3%;  Pred. No. 1.7e-05;
  Matches   63;  Conservative   34;  Mismatches   89;  Indels   45;  Gaps   11;

Qy         27 CLIGA---------VNLKSSNR-----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ 71
              |::|          ||:|    :       |  |||    | : |: |  :|  | | ||
Db         96 CVVTAEDGTESEATVNVKIFQKLMFKNAPTPQEFREGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                    :   |  :: |:  |  :|     |:|  : :  |   ||||  ::||    ||:
Db        153 -----HKGRDVILKKDV--RFIVLTNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |:: | | |      :  |     :|:  || |  :|| | |  || ::   :  :
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-NAEGFPEPTVSWTKDGEQIENEEDEK 261

Qy        188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
              | : ||        |    | |:|  :| ||| | ||     ||:  ::
Db        262 YLFSDDSSE-------LTIRKVDKNDEAEYVCIAENKAG-----EQDASIH 300


RESULT 15
T29757
protein UNC-89 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999
C;Accession: T29757
R;Du, Z.; Le, T.T.; Wilson, R.
submitted to the EMBL Data Library, May 1997
A;Description: The sequence of C. elegans cosmid C09D1.
A;Reference number: Z20679
A;Accession: T29757
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6642 <DUZ>
A;Cross-references: EMBL:AF003131; PIDN:AAB54132.1; GSPDB:GN00019; CESP:unc-89
A;Experimental source: strain Bristol N2; clone C09D1
C;Genetics:
A;Gene: CESP:unc-89
A;Map position: 1
A;Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2; 454/1; 500/1; 537/1; 6
/3; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1

  Query Match             9.9%;  Score 162.5;  DB 2;  Length 6642;
  Best Local Similarity   21.6%;  Pred. No. 0.00024;
  Matches   71;  Conservative   39;  Mismatches   93;  Indels  125;  Gaps   12;

Qy         45 EFESVELSCIITDSQTS----------DPRIEWKK--IQDEQTTYVFFDNKIQGDLAGRA 92
              ||  :  || :|: | :           |:|:| |   : | :  |  ::|  | |
Db       3828 EPVELLRSCTVTEKQQAILKCKVKGEPRPKIKWTKEGKEVEMSARVRAEHKDDGTL---- 3883

Qy         93 EILGKTSLKIWNVTRRDSALYRCE-------------VVARNDRKEIDEIVIELTVQVK 138
                    :|   |||: |:  ||||              :|      :||    :    ||
Db       3884 ------TLTFDNVTQADAGEYRCEAENEYGSAWTEGPIIVTLEGAPKIDGEAPDFLQPVK 3937

Qy        139 PVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLN 198
              |          | ||: | |  : | |:|   ||:|   |        |  |    :|:
Db       3938 PA--------VVTVGETAVLEGKIS-GKPKPSVKWYKNGEEL------KPSDRVKIENLD 3982

Qy        199 SETGTLVFTAVHKDDSGQYYCIASNDAG-------------------------SARCEEQ 233
              |  |  |     ||  :| | |||: |                          : : :|
Db       3983 DGTQRLTVTNAKLDDMDEYRCEASNEFGDVWSDVTLTVKEPAQVAPGFFKELSAIQVKET 4042

Qy        234 EMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKP----- 288
              |   ::  : |                                    | |  : :|: | |
Db       4043 ETAKFECKVSG----------------------------TKPDVKWFKD-GTPLKEDK 4071

Qy        289 --------DGVNYI-----RTDEEGDFR 303
                     ||   :     :||::|::|
Db       4072 RVHFESTDDGTQRLVIEDSKTDDQGNYR 4099


Search completed: April 12, 2004, 09:16:45
Job time : 22 secs
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R;Adachi, M.; Sekiya, M.; Arimura, Y.; Takekawa, M.; Itoh, F.; Hinoda, Y.; Imai, K.; Yac
Cancer Res. 52, 737-740, 1992
A;Title: Protein-tyrosine phosphatase expression in pre-B cell NALM-6.
A;Reference number: A44929; MUID:92119637; PMID:1370651
A;Accession: B44929
A;Molecule type: mRNA
A;Residues: 1756-1804,'C',1806-1845 <ADA>
A;Cross-references: GB:S78086; NID:g243545; PIDN:AAB21147.1; PID:g243546
A;Experimental source: pre-B cell NALM-6
A;Note: sequence extracted from NCBI backbone (NCBIN:78086, NCBIP:78087)
A;Note: the authors did not report the entire codon for residue 90
C;Genetics:
A;Gene: GDB:PTPRD
A;Cross-references: GDB:131384; OMIM:601598
A;Map position: 9p24-9p24
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
ogy
C;Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
F;38-100/Domain: immunoglobulin homology <IMM1>
F;140-209/Domain: immunoglobulin homology <IMM2>
F;250-304/Domain: immunoglobulin homology <IMM3>
F;711-811/Domain: fibronectin type III repeat homology <3FR>
F;1293-1912/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1669-1892/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1553/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1559/Binding site: substrate phosphate (Arg) #status predicted
F;1844/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1850/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             10.4%;  Score 169.5;  DB 2;  Length 1912;
  Best Local Similarity   28.6%;  Pred. No. 1.4e-05;
  Matches   65;  Conservative   35;  Mismatches   76;  Indels   51;  Gaps   13;

Qy          39 RTPVVQEFESVELSCIITDSQTSDPR--IEW----KKIQDEQTTYVFFDNKIQGDLAGRA 92
               |||| |    |  ::  |  : | |||  | |     ||: :::   : ||:       |
Db          28 RTPVDQTGVSGGVASFICQA-TGDPRPKIVWNKKGKKVSNQRFEVIEFDD-------GSG 79

Qy          93 EILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPV 152
                :|     |:    | || |:| |  || |:  ||  :   ||| :      ::|:  |
Db          80 SVLRIQPLR----TPRDEAIYEC--VASNNVGEI-SVSTRLTVLRED-----QIPRGFPT 127

Qy         153 GKM------------ATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLNSE 200
                |              ||: |  | |:| |  :|::: :|: | |  | | :     | ||
Db         128 IDMGPQLKVVERTRTATMLCAAS-GNPDPEITWFKDFLPVDT-SNNNGRIK----QLRSE 181

Qy         201 T-------GTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
               :       | |       : | |:| |:|:| ||:       : | :|
Db         182 SIGGTPIRGALQIEQSEESDQGKYECVATNSAGTRYSAPANLYVREL 228


RESULT 12
A39712
kinase-like protein klg precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 24-Sep-1999
C;Accession: A39712
R;Chou, Y.H.; Hayman, M.J.
Proc. Natl. Acad. Sci. U.S.A. 88, 4897-4901, 1991
A;Title: Characterization of a member of the immunoglobulin gene superfamily that possib
A;Reference number: A39712; MUID:91271300; PMID:1711213
A;Accession: A39712
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1051 <CHO>
A;Cross-references: GB:M63437; NID:g212235; PIDN:AAA48933.1; PID:g212236
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C;Keywords: ATP
F;775-1046/Domain: protein kinase homology <KIN>
F;783-791/Region: protein kinase ATP-binding motif

  Query Match             10.1%;  Score 164.5;  DB 2;  Length 1051;
  Best Local Similarity   24.5%;  Pred. No. 1.8e-05;
  Matches   66;  Conservative   35;  Mismatches  109;  Indels   59;  Gaps   11;

Qy          40 TPVVQEFESVE------LSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAE 93
               ||  |  : :|       :||  |  :   | |:| |             : :  :: ||
Db         486 TPPPQPLQCMEFNKEVTVSCSATGRE--KPTIQWTKTD---------GSSLPSHVSHRAG 534

Qy          94 ILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVG 153
               |      |    |:| ||  | |  :| |  :       ::| | |     :   |  |  |
Db         535 I-----LSFHKVSRSDSGNYTC--IASNSPQGEIRATVQLVVAVYVTFKLEPEPTTVYQG 587

Qy         154 KMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDD 213
               |   || :|| | ||  |   |  |  |:  || :   :      |:||  |  | :|
Db         588 HTAMFQCQ-AEGDPVPHIQWKGKDKIL-DPSKLLPRIQIMPN------GSLVIYDVTTED 639

Qy         214 SGQYYCIASNDAG----------SARCEEQE---------MEVYDLNIGGIIGGVLV 251
               ||:| |||  |                || |          ::   |::|  :  :::
Db         640 SGKYTCIAGNSCNIKHREAFLYVVDKPAAEEDEGPSSHTPYKMIQTIGLSVGAAVAYIII 699

Qy         252 VLAVLALITLGICCAYRRGYFINNKQDGE 280
               || ::      |   |:   :  :||
Db         700 VLGLMF-----YCKKRRKAKRLKKHPEGE 723


RESULT 13
S18252
heparan sulfate proteoglycan - mouse
N;Alternate names: perlecan
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C;Accession: S18252; A31917; B31917; S66460
R;Noonan, D.M.; Fulle, A.; Valente, P.; Cai, S.; Horigan, E.; Sasaki, M.; Yamada, Y.; Ha
J. Biol. Chem. 266, 22939-22947, 1991
A;Title: The complete sequence of perlecan, a basement membrane heparan sulfate proteogly
adhesion molecule.
A;Reference number: S18252; MUID:92078153; PMID:1744087
A;Accession: S18252
A;Molecule type: mRNA
A;Residues: 1-3707 <NOO>
A;Cross-references: EMBL:M77174; NID:g200295; PIDN:AAA39911.1; PID:g200296
R;Noonan, D.M.; Horigan, E.A.; Ledbetter, S.R.; Vogeli, G.; Sasaki, M.; Yamada, Y.; Hasse
J. Biol. Chem. 263, 16379-16387, 1988
A;Title: Identification of cDNA clones encoding different domains of the basement membrar
A;Reference number: A92680; MUID:89034110; PMID:2972708
A;Accession: A31917
A;Molecule type: mRNA
A;Residues: 940-1601 <NO2>
A;Cross-references: GB:J04054; NID:g200252; PIDN:AAA39899.1; PID:g200253
A;Accession: B31917
A;Molecule type: mRNA
A;Residues: 1870-2600 <NO3>
A;Cross-references: GB:J04055; NID:g200300; PIDN:AAA39912.1; PID:g200301
R;Schulze, B.; Mann, K.; Battistutta, R.; Wiedemann, H.; Timpl, R.
Eur. J. Biochem. 231, 551-556, 1995
A;Title: Structural properties of recombinant domain III-3 of perlecan containing a globu
A;Reference number: S66460; MUID:95377282; PMID:7649154
A;Accession: S66460
A;Molecule type: protein
A;Residues: 1272-1274,'X',1276,'X',1278-1279 <SCH>
C;Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G repe
C;Keywords: glycoprotein
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;764-811/Domain: laminin-type EGF-like homology <LEG>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG7>
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>
F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>
F;3163-3198/Domain: EGF homology <EGF>
F;3270-3423/Domain: laminin G repeat homology <LG2>
F;3464-3492/Domain: EGF homology <EGF7>
F;1256,1891,2336,2394,2427/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             10.1%;  Score 164.5;  DB 2;  Length 3707;
```

C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1115/Product: neural cell adhesion molecule, long domain splice form #status experi
F;20-809,1077-1115/Product: neural cell adhesion molecule, short domain splice form #sta
F;20-711/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;262-272/Region: NCAM binding #status predicted
F;323-388/Domain: immunoglobulin homology <IMM4>
F;420-482/Domain: immunoglobulin homology <IMM5>
F;519-596/Domain: fibronectin type III repeat homology <FN3A>
F;625-685/Domain: fibronectin type III repeat homology <FN3B>
F;712-729/Domain: transmembrane #status predicted <TMM>
F;730-1115/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F;222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.5%; Score 171.5; DB 1; Length 1115;
Best Local Similarity 27.3%; Pred. No. 5.1e-06;
Matches 63; Conservative 41; Mismatches 84; Indels 43; Gaps 12;

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Qy         27 CLIGA---------VNLKSSNR-----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ 71
Db         96 CVVTAEDGTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
Db        153 -----HKGRDVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEE-D 260

Qy        188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
Db        261 ERSRSSV----SDSSEVTIRNVDKNDEAEYVCIAENKAG-----EQDASIH 302
```

RESULT 10
IJRTNC
neural cell adhesion molecule short domain form precursor - rat
N;Alternate names: NCAM-140
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C;Accession: S00846; B37795; I58136
R;Small, S.J.; Shull, G.E.; Santoni, M.J.; Akeson, R.
J. Cell Biol. 105, 2335-2345, 1987
A;Title: Identification of a cDNA clone that contains the complete coding sequence for a
A;Reference number: S00846; MUID:88059265; PMID:3680385
A;Accession: S00846
A;Molecule type: mRNA
A;Residues: 1-858 <SMA>
A;Cross-references: EMBL:X06564
R;Small, S.J.; Akeson, R.
J. Cell Biol. 111, 2089-2096, 1990
A;Title: Expression of the unique NCAM VASE exon is independently regulated in distinct
A;Reference number: A37795; MUID:91035620; PMID:1699951
A;Accession: B37795
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 340-381 <SM2>
R;Small, S.J.; Haines, S.L.; Akeson, R.A.
Neuron 1, 1007-1017, 1988
A;Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev
A;Reference number: I58136; MUID:90166485; PMID:2483093
A;Accession: I58136
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 355-364 <RFS>

A;Cross-references: GB:M32611; NID:g205643; PIDN:AAA41679.1; PID:g205644
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Various forms of NCAM are produced by alternative splicing.
C;Genetics:
A;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-858/Product: neural cell adhesion molecule, short domain form #status predicted <MA
F;20-721/Domain: extracellular #status predicted <EXT>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;263-272/Region: NCAM binding #status predicted
F;323-398/Domain: immunoglobulin homology <IMM4>
F;430-492/Domain: immunoglobulin homology <IMM5>
F;529-606/Domain: fibronectin type III repeat homology <FN3A>
F;635-695/Domain: fibronectin type III repeat homology <FN3B>
F;722-739/Domain: transmembrane #status predicted <TMM>
F;740-858/Domain: intracellular #status predicted <INT>
F;41-96,139-189,235-288,330-396,437-490/Disulfide bonds: #status predicted
F;222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.4%; Score 170.5; DB 1; Length 858;
Best Local Similarity 26.3%; Pred. No. 4.5e-06;
Matches 61; Conservative 41; Mismatches 85; Indels 45; Gaps 12;

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Qy         27 CLIGA---------VNLKSSNR-----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ 71
Db         96 CVVTAEDGTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
Db        153 -----HKGRDVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEE--- 258

Qy        188 PRFRNSSSHL-NSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
Db        259 ---EDDEKHIFSDDSSELTIRNVDKNDEAEYVCIAENKAG-----EQDASIH 302
```

RESULT 11
A56178
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - human
N;Alternate names: protein-tyrosine-phosphatase BPTP-2
C;Species: Homo sapiens (man)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 21-Jan-2000
C;Accession: A56178; S12052; B44929
R;Pulido, R.; Krueger, N.X.; Serra-Pages, C.; Saito, H.; Streuli, M.
J. Biol. Chem. 270, 6722-6728, 1995
A;Title: Molecular characterization of the human transmembrane protein-tyrosine phosphat
ase delta isoforms.
A;Reference number: A56178; MUID:95204468; PMID:7896816
A;Accession: A56178
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1912 <PUL>
A;Cross-references: GB:L38929; NID:g755652; PIDN:AAC41749.1; PID:g755653
R;Krueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
A;Title: Structural diversity and evolution of human receptor-like protein tyrosine phos
A;Reference number: S12049; MUID:91006018; PMID:2170109
A;Accession: S12052
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 390-1912 <KRU>
A;Cross-references: GB:X54133; NID:g35789; PIDN:CAA38068.1; PID:g35790
A;Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-T

```
  Best Local Similarity   29.5%;  Pred. No. 1.7e-06;
  Matches   62;  Conservative   28;  Mismatches   86;  Indels   34;  Gaps   11;

Qy         30 GAVNLKSSNR-----TPVVQEFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN 82
              |||||   :       |  |||   | : || |  :| |  | |: | :|     | ||
Db        105 GTVNLKIYQKLTFKYAPTPQEFTEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159

Qy         83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEIVIELTVQVKPV 140
              :     |  :|    |:|  : : |   ||||  ::||    ||:   |:: | | | |:
Db        160 DV------RFVVLANNYLQIRGIKKTDEGNYRCEGRILARG---EINYKDIQVIVNVPPL 210

Qy        141 TPV--CRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLN 198
              ||     : :   | | :::| | |  || :   |:  |       |              |
Db        211 IQARQIRVNATANMDESVVLSC-DADGFPDPEISWLKKGEPI-EDGEEKISF-------N 261

Qy        199 SETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
                :   :   | |:|  :| |||:| || |
Db        262 EDKSEMTIYRVEKEDEAEYSCIANNQAGEA 291


RESULT 8
IJMSNG
neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse
N;Alternate names: NCAM-120
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000
C;Accession: A29673; S00382; A44290
R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec
EMBO J. 6, 907-914, 1987
A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A;Reference number: A29673; MUID:87246524; PMID:3595563
A;Accession: A29673
A;Molecule type: mRNA
A;Residues: 1-725 <BAR>
A;Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A;Title: Differential splicing and alternative polyadenylation generates distinct NCAM t
A;Reference number: S00382; MUID:88283628; PMID:3396534
A;Accession: S00382
A;Molecule type: DNA
A;Residues: 642-656,'D',658-725 <BA2>
A;Cross-references: EMBL:X07195
R;Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of m
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: A44290
A;Molecule type: protein
A;Residues: 20-36 <ROU>
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMS
C;Genetics:
A;Gene: NCAM
A;Map position: 9
A;Introns: 701/1
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane
F;1-19/Domain: signal sequence #status predicted <SIG>
F;34-98/Domain: immunoglobulin homology <IMM1>
F;132-191/Domain: immunoglobulin homology <IMM2>
F;152-156/Region: heparin binding #status predicted
F;161-165/Region: heparin binding #status predicted
F;228-290/Domain: immunoglobulin homology <IMM3>
F;263-272/Region: NCAM binding #status predicted
F;323-388/Domain: immunoglobulin homology <IMM4>
F;420-482/Domain: immunoglobulin homology <IMM5>
F;519-596/Domain: fibronectin type III repeat homology <FN3A>
F;625-685/Domain: fibronectin type III repeat homology <FN3B>
F;41-96,139-189,235-288,330-386,427-480/Disulfide bonds: #status predicted
F;222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             10.5%;  Score 171.5;  DB 1;  Length 725;
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```
  Best Local Similarity   27.3%;  Pred. No. 3e-06;
  Matches   63;  Conservative   41;  Mismatches   84;  Indels   43;  Gaps   12;

Qy         27 CLIGA---------VNLKSSNR-----TPVVQEFESVELSCIITDSQTS-DPRIEWKKIQ 71
              |:: |          ||:|   :      |  |||:  | : |: |  :|  | | ||
Db         96 CVVTAEDGTQSEATVNVKIFQKLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWK--- 152

Qy         72 DEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEI 129
                 :   |  :: |:  |  :|    |:|  : : |   ||||  ::||    ||:
Db        153 -----HKGRDVILKKDV--RFIVLSNNYLQIRGIKKTDEGTYRCEGRILARG---EINFK 202

Qy        130 VIELTVQVKPVTPVCR--VPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |:: | | |     :  |     :|:  || | :::| | |  || ::  |:  :  :
Db        203 DIQVIVNVPPTVQARQSIVNATANLGQSVTLVC-DADGFPEPTMSWTKDGEPIENEEE-D 260

Qy        188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVY 238
              | |:|     |::  :    | |:|  :| ||| | ||     ||:  ::
Db        261 ERSRSSV----SDSSEVTIRNVDKNDEAEYVCIAENKAG-----EQDASIH 302


RESULT 9
IJMSNL
neural cell adhesion molecule 1 precursor, long domain splice form - mouse
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain splice form (NCAM-140)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Dec-2000
C;Accession: A29673; S00844; S00384; A28281; A44290; S00383
R;Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fonteci
EMBO J. 6, 907-914, 1987
A;Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000
A;Reference number: A29673; MUID:87246524; PMID:3595563
A;Accession: A29673
A;Molecule type: mRNA
A;Residues: 1-548,'T',550-571,'T',573-574,'D',576-588,'MQPS',593,'S',595-599,'P',601,'L',
A;Cross-references: EMBL:Y00051; NID:g53342; PIDN:CAA68263.1; PID:g53343
R;Santoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.; Wi
Nucleic Acids Res. 15, 8621-8641, 1987
A;Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse neura
A;Reference number: S00844; MUID:88067687; PMID:3684567
A;Accession: S00844
A;Molecule type: mRNA
A;Residues: 529-809,1077-1115 <SAN>
A;Cross-references: EMBL:X06328; NID:g53322; PIDN:CAA29641.1; PID:g817984
R;Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.
EMBO J. 7, 625-632, 1988
A;Title: Differential splicing and alternative polyadenylation generates distinct NCAM ti
A;Reference number: S00382; MUID:88283628; PMID:3396534
A;Accession: S00384
A;Molecule type: DNA
A;Residues: 642-1115 <BAR>
A;Cross-references: EMBL:X07195
R;Barthels, D.; Vopper, G.; Wille, W.
Nucleic Acids Res. 16, 4217-4225, 1988
A;Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse, i
A;Reference number: A28281; MUID:88247737; PMID:2454455
A;Accession: A28281
A;Molecule type: mRNA
A;Residues: 804-1081 <BA3>
A;Cross-references: EMBL:X07244; NID:g53321; PIDN:CAA30230.1; PID:g929720
R;Rougon, G.; Marshak, D.R.
J. Biol. Chem. 261, 3396-3401, 1986
A;Title: Structural and immunological characterization of the amino-terminal domain of ma
A;Reference number: A44290; MUID:86140120; PMID:3512556
A;Accession: A44290
A;Molecule type: protein
A;Residues: 20-36 <ROU>
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mole
C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMSN
C;Genetics:
A;Gene: NCAM
A;Map position: 9
A;Introns: 643/3; 701/1; 770/2; 809/2; 1076/2
```

```
F;1542/Binding site: substrate phosphate (Arg) #status predicted
F;1826/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1832/Binding site: substrate phosphate (Arg) #status predicted

  Query Match             11.0%;  Score 180.5;  DB 2;  Length 1894;
  Best Local Similarity   28.8%;  Pred. No. 1.7e-06;
  Matches   72;  Conservative   34;  Mismatches   75;  Indels   69;  Gaps   15;

Qy          3 LRRPPRLRL------CARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIIT 56
              :|||  | |       ||  |  |                    ||||  |   |  ::  |
Db         11 VRRPLSLLLTFFLCACAETPPRF-----------------TRTPVDQTGVSGGVASFIC 52

Qy         57 DSQTSDPR--IEW----KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDS 110
               : | |||  | |     ||: :::   : ||:       |   :|    |:    | ||
Db         53 QA-TGDPRPKIVWNKKGKKVSNQRFEVIEFDD-------GSGSVLRIQPLR----TPRDE 100

Qy        111 ALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKM-----------ATL 158
              |:| |  || |:  ||  :   |||  :      ::|:  |   |             ||:
Db        101 AIYEC--VASNNVGEI-SVSTRLTVLRED-----QIPRGFPTIDMGPQLKVVERTRTATM 152

Qy        159 HCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLNSET-GTLVFTAVHKDDSGQY 217
              |  | |:| |  :|::: :|: | |  | | :     | ||: | |      : | |:|
Db        153 LCAAS-GNPDPEITWFKDFLPVDT-SNNNGRIK----QLRSESIGALQIEQSEESDQGKY 206

Qy        218 YCIASNDAGS 227
              |:|:| ||:
Db        207 ECVATNSAGT 216


RESULT 5
A31923
amalgam protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jul-2000
C;Accession: A31923
R;Seeger, M.A.; Haffley, L.; Kaufman, T.C.
Cell 55, 589-600, 1988
A;Title: Characterization of amalgam: a member of the immunoglobulin superfamily from Dr
A;Reference number: A31923; MUID:89028670; PMID:3141062
A;Accession: A31923
A;Molecule type: DNA
A;Residues: 1-333 <SEE>
A;Cross-references: GB:M23561; NID:g156920; PIDN:AAA28367.1; PID:g156921
C;Genetics:
A;Gene: FlyBase:Ama
A;Cross-references: FlyBase:FBgn0000071

  Query Match             11.0%;  Score 180;  DB 2;  Length 333;
  Best Local Similarity   26.8%;  Pred. No. 2.3e-07;
  Matches   52;  Conservative   39;  Mismatches   83;  Indels   20;  Gaps    5;

Qy         35 KSSNRTPVVQEFESVELSCIITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEI 94
              ::: :: :| | :::||:|    :    | | | :           :   :     :
Db        143 ENTPKSTLVTEGQNLELTC--HANGFPKPTISWAR-----------EHNAVMPAGGHL 187

Qy         95 LGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGK 154
              | : :|:| :| | |    | |  :|:|    : |: :| : |: :|   | |    |  |
Db        188 LAEPTLRIRSVHRMDRGGYYC--IAQNGEGQPDKRLIRVEVEFRPQIAVQRPKIAQMVSH 245

Qy        155 MATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDS 214
              | | |    :|:| |   |::| |||    |  :    |::|   : |   |    :| ::|
Db        246 SAELEC-SVQGYPAPTVVWHKNGVPL--QSSRHHEVANTASSSGTTTSVLRIDSVGEEDF 302

Qy        215 GQYYCIASNDAGSA 228
              | ||| |:|  | |
Db        303 GDYYCNATNKLGHA 316


RESULT 6
JE0100
neural cell adhesion molecule 2 - African clawed frog
N;Alternate names: N-CAM 2
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: JE0100
R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the ma
A;Reference number: JE0099; MUID:98204770; PMID:9535795
A;Accession: JE0100
A;Molecule type: mRNA
A;Residues: 1-725 <KUD>
A;Cross-references: DDBJ:AB008163; NID:g3116228; PIDN:BAA25932.1; PID:g3116229
A;Experimental source: heart
C;Comment: This protein mediates and regulates various cell-cell interactions through bo
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
F;413-475/Domain: immunoglobulin homology <IMM>
F;512-589/Domain: fibronectin type III repeat homology <3FR>

  Query Match             10.8%;  Score 177;  DB 2;  Length 725;
  Best Local Similarity   29.5%;  Pred. No. 1.1e-06;
  Matches   62;  Conservative   28;  Mismatches   86;  Indels   34;  Gaps   11;

Qy         30 GAVNLKSSNR-----TPVVQEFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN 82
              | ||||   :       |  |||   | : || |  :| | | | |: | : :|     | |
Db        105 GTVNLKIYQKLTFKYAPTPQEFTEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159

Qy         83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARNDRKEIDEIVIELTVQVKPV 140
               :       |  :|     |:|  : : |    ||||  ::||     ||:   |:: | | |:
Db        160 DV------RFVVLANNYLQIRGIKKTDEGNYRCEGRILARG---EINYKDIQVIVNVPPL 210

Qy        141 TPV--CRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHLN 198
                ||      : :    | | :::| | |  | ||  :   |:  |       |       |
Db        211 IQARQIRVNATANMDESVVLSC-DADGFPDPEISWLKKGEPI-EDGEEKISF-------N 261

Qy        199 SETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
               :   :    | |:|  :| |||:| | | |
Db        262 EDKSEMTIYRVEKEDEAEYSCIANNQAGEA 291


RESULT 7
JN0635
neural cell adhesion molecule 2 precursor - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
C;Accession: JN0635
R;Tonissen, K.F.; Krieg, P.A.
Gene 127, 243-247, 1993
A;Title: Two neural-cell adhesion molecule(NCAM)-encoding genes in Xenopus laevis are ex
A;Reference number: JN0635; MUID:93273239; PMID:7684721
A;Accession: JN0635
A;Molecule type: mRNA
A;Residues: 1-1092 <TON>
A;Cross-references: GB:M76710; NID:g214611; PIDN:AAA49910.1; PID:g214612
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Genetics:
A;Gene: NCAM2
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; cell adhesion; duplication; heparin binding; sialoglyc
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1092/Product: neural cell adhesion molecule 2 #status predicted <NCA>
F;20-705/Domain: extracellular #status predicted <EXT>
F;34-95/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;317-381/Domain: immunoglobulin homology <IMM3>
F;413-475/Domain: immunoglobulin homology <IMM4>
F;512-589/Domain: fibronectin type III repeat homology <FN3A>
F;619-680/Domain: fibronectin type III repeat homology <FN3B>
F;706-723/Domain: transmembrane #status predicted <TMM>
F;724-1092/Domain: intracellular #status predicted <INT>
F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F;219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             10.8%;  Score 177;  DB 1;  Length 1092;
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Db        241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy        303 RHKSSFVI 310
              :  |||::
Db        292 KQTSSFLV 299


RESULT 2
JE0099
neural cell adhesion molecule 1 - African clawed frog
N;Alternate names: N-CAM 1
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: JE0099
R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the ma
A;Reference number: JE0099; MUID:98204770; PMID:9535795
A;Accession: JE0099
A;Molecule type: mRNA
A;Residues: 1-725 <KUD>
A;Cross-references: DDBJ:AB008162; NID:g3116226; PIDN:BAA25931.1; PID:g3116227
A;Experimental source: heart
C;Comment: This protein mediates and regulates various cell-cell interactions through bo
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
F;413-475/Domain: immunoglobulin homology <IMM>
F;512-589/Domain: fibronectin type III repeat homology <3FR>

  Query Match             11.4%;  Score 187;  DB 2;  Length 725;
  Best Local Similarity   29.9%;  Pred. No. 1.6e-07;
  Matches   63;  Conservative   30;  Mismatches   82;  Indels   36;  Gaps   12;

Qy         30 GAVNLK-----SSNRTPVVQEFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN 82
              | ||||     :    |  |||:  | : || |  :| |  | |: | :|      | |
Db        105 GTVNLKIYQKLTFKNAPTPQEFKEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159

Qy         83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARND--RKEIDEIV-IELTVQV 137
              :       |  :|     |:|  : : |    ||||  ::|| :   |:|  || :  |:|
Db        160 DV------RFVVLANNYLQIRGIKKTDEGTYRCEGRILARGEINYKDIQVIVNVPPTIQA 213

Qy        138 KPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHL 197
              : :    ||      : :   | | :::| | |  || :   |:  |       |
Db        214 RQL----RVNATAKMAESVVLSC-DADGFPDPEISWLKKGEPI-EDGEEKISF------- 260

Qy        198 NSETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
              | :   :    | |||  :| |||:| || |
Db        261 NEDQSEMTIHHVEKDDEAEYSCIANNQAGEA 291


RESULT 3
IJXLNL
neural cell adhesion molecule long domain form precursor - African clawed frog
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999
C;Accession: S09600
R;Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Acids Res. 17, 10321-10335, 1989
A;Title: Primary structure and developmental expression of a large cytoplasmic domain fo
A;Reference number: S09600; MUID:90098871; PMID:2481269
A;Accession: S09600
A;Molecule type: mRNA
A;Residues: 1-1088 <KRI>
A;Cross-references: EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g214610
A;Note: the authors translated the codon AAA for residue 970 as Leu
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C;Comment: Several forms of NCAM are produced by alternative splicing.
C;Genetics:
A;Gene: NCAM
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <LDI
F;20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status prec
F;20-705/Domain: extracellular #status predicted <EXT>
F;34-95/Domain: immunoglobulin homology <IMM1>
F;129-188/Domain: immunoglobulin homology <IMM2>
F;149-153/Region: heparin binding #status predicted
F;158-162/Region: heparin binding #status predicted
F;225-284/Domain: immunoglobulin homology <IMM3>
F;317-381/Domain: immunoglobulin homology <IMM4>
F;413-475/Domain: immunoglobulin homology <IMM5>
F;512-589/Domain: fibronectin type III repeat homology <FN3A>
F;618-679/Domain: fibronectin type III repeat homology <FN3B>
F;706-723/Domain: transmembrane #status predicted <TMM>
F;724-1088/Domain: intracellular #status predicted <INT>
F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F;219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             11.4%;  Score 186;  DB 1;  Length 1088;
  Best Local Similarity   29.9%;  Pred. No. 3.1e-07;
  Matches   63;  Conservative   30;  Mismatches   82;  Indels   36;  Gaps   12;

Qy         30 GAVNLK-----SSNRTPVVQEFESVELSCIITDSQTSDPR-IEWK-KIQDEQTTYVFFDN 82
              | ||||     :    |  |||:  | : || |  :| |  | |: | :|      | |
Db        105 GTVNLKIYQKLTFKNAPTPQEFKEGEDAVIICDVSSSIPSIITWRHKGKD-----VIFKK 159

Qy         83 KIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCE--VVARND--RKEIDEIV-IELTVQV 137
              :       |  :|     |:|  : : |    ||||  ::|| :   |:|  || :  |:|
Db        160 DV------RFVVLANNYLQIRGIKKTDEGTYRCEGRILARGEINYKDIQVIVNVPPTIQA 213

Qy        138 KPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSSHL 197
              : :    ||      : :   | | :::| | |  || :   |:  |       |
Db        214 RQL----RVNATANMAESVVLSC-DADGFPDPEISWLKKGEPI-EDGEEKISF------- 260

Qy        198 NSETGTLVFTAVHKDDSGQYYCIASNDAGSA 228
              | :   :    | |||  :| |||:| || |
Db        261 NEDQSEMTIHHVEKDDEAEYSCIANNQAGEA 291


RESULT 4
C54689
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta, splice form B precursor
N;Alternate names: MPTP delta type B/C
N;Contains: protein tyrosine phosphatase, receptor type delta, splice form C
C;Species: Mus musculus (house mouse)
C;Date: 25-Apr-1995 #sequence_revision 19-May-1995 #text_change 12-Feb-1999
C;Accession: C54689; B54689
R;Mizuno, K.; Hasegawa, K.; Katagiri, T.; Ogimoto, M.; Ichikawa, T.; Yakura, H.
Mol. Cell. Biol. 13, 5513-5523, 1993
A;Title: MPTP delta, a putative murine homolog of HPTP delta, is expressed in specialized
A;Reference number: A54689; MUID:93360986; PMID:8355697
A;Accession: C54689
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1894 <MIZ>
A;Experimental source: brain; splice form B
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:137486, NCBIP:137487)
A;Accession: B54689
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-352,'H',354-535,'S',537-601,1002-1894 <MI2>
A;Experimental source: brain; splice form C
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:136527, NCBIP:136530)
C;Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; i
ogy
C;Keywords: alternative splicing; glycoprotein; phosphoprotein; phosphoric monoester hydr
F;45-107/Domain: immunoglobulin homology <IMM1>
F;245-299/Domain: immunoglobulin homology <IMM2>
F;317-399/Domain: fibronectin type III repeat homology <FN3A>
F;1278-1894/Domain: leukocyte common antigen cytosolic domain homology <LAC>
F;1652-1874/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1536/Active site: Cys (phosphocysteine intermediate) #status predicted
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:12:38 ; Search time 20 Seconds
(without alignments)
1490.969 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 1635
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	419	25.6	299	2	S56749	junctional adhesio
2	187	11.4	725	2	JE0099	neural cell adhesi
3	186	11.4	1088	1	IJXLNL	neural cell adhesi
4	180.5	11.0	1894	2	C54689	protein-tyrosine-p
5	180	11.0	333	2	A31923	amalgam protein pr
6	177	10.8	725	2	JE0100	neural cell adhesi
7	177	10.8	1092	1	JN0635	neural cell adhesi
8	171.5	10.5	725	1	IJMSNG	neural cell adhesi
9	171.5	10.5	1115	1	IJMSNL	neural cell adhesi
10	170.5	10.4	858	1	IJRTNC	neural cell adhesi
11	169.5	10.4	1912	2	A56178	protein-tyrosine-p
12	164.5	10.1	1051	2	A39712	kinase-like protei
13	164.5	10.1	3707	2	S18252	heparan sulfate pr
14	163.5	10.0	853	1	IJBONC	neural cell adhesi
15	162.5	9.9	6642	2	T29757	protein UNC-89 - C
16	161.5	9.9	1612	2	T30805	dutt1 protein - mo
17	161	9.8	7962	2	I38346	elastic titin - hu
18	159.5	9.8	1033	2	S19247	cell adhesion prot
19	159	9.7	538	2	JC2457	vascular cell adhe
20	159	9.7	1323	2	PN0568	connectin 3B - chi
21	159	9.7	4162	2	T42633	connectin/titin -
22	157	9.6	1907	2	S50893	protein-tyrosine-p
23	156	9.5	1091	1	IJCHNL	neural cell adhesi
24	156	9.5	1501	2	I58148	protein-tyrosine-p
25	156	9.5	1863	2	S46217	protein-tyrosine-p
26	155.5	9.5	761	1	IJHUNG	neural cell adhesi
27	155.5	9.5	1259	2	A43425	Bravo/Nr-CAM cell
28	155.5	9.5	1268	1	A39640	neural cell adhesi
29	154.5	9.4	495	2	T25750	hypothetical prote
30	153.5	9.4	365	2	JC7780	coxsackie- and ade
31	153	9.4	352	2	T33433	hypothetical prote
32	153	9.4	875	2	T33434	hypothetical prote
33	152	9.3	483	2	T17346	hypothetical prote
34	151	9.2	1651	2	T14160	transmembrane rece
35	150.5	9.2	702	2	A36319	carcinoembryonic a
36	150	9.2	1262	1	B48758	protein-tyrosine-p
37	150	9.2	1496	1	A48758	protein-tyrosine-p
38	149.5	9.1	1897	1	TDHULK	leukocyte antigen-
39	149	9.1	521	2	S34338	biliary glycoprote
40	149	9.1	1898	2	S46216	leukocyte antigen-
41	148.5	9.1	646	2	I38049	cell surface glyco
42	147.5	9.0	871	1	I48696	protein-tyrosine k
43	147.5	9.0	881	1	I48697	protein-tyrosine k
44	147	9.0	338	2	JC5519	50K glycoprotein p
45	147	9.0	344	2	I56551	neurotrimin - rat

ALIGNMENTS

RESULT 1
S56749
junctional adhesion molecule precursor - human
N;Alternate names: F11 platelet antigen; platelet adhesion molecule PAM-1; platelet F11
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: A59406; S56749
R;Ozaki, H.; Ishii, K.; Horiuchi, H.; Arai, H.; Kawamoto, T.; Okawa, K.; Iwamatsu, A.; K
J. Immunol. 163, 553-557, 1999
A;Title: Cutting edge: combined treatment of TNF-alpha and IFN-gamma causes redistributi
A;Reference number: A59406; MUID:99323940; PMID:10395639
A;Accession: A59406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-299 <OZA>
A;Cross-references: GB:AAD42050; NID:g5326797; PIDN:AAD42050.1
R;Naik, U.P.; Ehrlich, Y.H.; Kornecki, E.
Biochem. J. 310, 155-162, 1995
A;Title: Mechanisms of platelet activation by a stimulatory antibody: cross-linking of a
A;Reference number: S56749; MUID:95374438; PMID:7646439
A;Accession: S56749
A;Molecule type: protein
A;Residues: 28-49,'X',51-53;62-73,'E',75-103;123,'F',125-130;'FDKDXTIYLNXY';'LT',206,'X'
A;Note: the order of the peptides other than the amino terminus was not determined
C;Genetics:
A;Gene: JAM
C;Keywords: glycoprotein; phosphoprotein; platelet aggregation; platelet membrane
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-299/Product: junctional adhesion molecule #status predicted <MAT>

Query Match 25.6%; Score 419; DB 2; Length 299;
Best Local Similarity 32.8%; Pred. No. 3.1e-27;
Matches 101; Conservative 47; Mismatches 138; Indels 22; Gaps 7;

```
Qy          8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
              |  ||      | | :|     :|:| : ||     : |   |:|||    |  | ||:||
Db          9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              |  | :  |  | ::|||      |   |  | :   :||| |:  | | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |: ::| | | |   :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
              | |||   ||  || ||| :   |:|:| | | |  |:          ||  : |:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
                |||  | :| ::  ||  || ||:|   |:   |   | |                ||:|
```

```
CC   ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC   ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC   antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC   activities, and can be used in gene therapy. The PRO polynucleotides,
CC   proteins, agonists and antagonists are useful for treating or diagnosing
CC   a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
CC   cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
CC   atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC   angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC   angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC   healing. The PRO polynucleotides have applications in molecular biology,
CC   including use as hybridisation probes, and in chromosome and gene
CC   mapping. ABL88259 to ABL88267 represent primers and probes used in the
CC   exemplification of the present invention
XX
SQ   Sequence 310 AA;

  Query Match           99.6%;  Score 1629;  DB 5;  Length 310;
  Best Local Similarity  99.7%;  Pred. No. 8.6e-131;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 15
ABG65297
ID   ABG65297 standard; protein; 310 AA.
XX
AC   ABG65297;
XX
DT   27-AUG-2002  (first entry)
XX
DE   Human albumin fusion protein #1972.
XX
KW   Albumin fusion protein; therapeutic protein X; human albumin; HA;
KW   human serum albumin; HSA; cancer; reproductive disorder;
KW   digestive disorder; immune disorder; endocrine disorder;
KW   haematopoietic disorder; neural disorder; connective disorder;
KW   cytostatic; antiinfertility; antiinflammatory; antiulcer;
KW   immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
KW   neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
KW   osteopathic; antiarthritic.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200177137-A1.
XX
PD   18-OCT-2001.
XX
PF   12-APR-2001; 2001WO-US011988.
XX
PR   12-APR-2000; 2000US-0229358P.
PR   25-APR-2000; 2000US-0199384P.
PR   21-DEC-2000; 2000US-0256931P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Haseltine WA;
XX
DR   WPI; 2002-010886/01.
XX
PT   New fusion protein for treating disease e.g. diabetes comprises an
PT   albumin fused to a therapeutic protein.
XX
PS   Claim 1; Page 1895; 2102pp; English.
XX
CC   The present invention relates to albumin fusion proteins comprising a
CC   therapeutic protein X and human albumin (HA, also known as human serum
CC   albumin, HSA). The proteins are useful for treating a disease or disorder
CC   that may be modulated by therapeutic protein X. The albumin extends the
CC   shelf-life of protein X, and may increase its biological in vitro/in vivo
CC   activity. The protein is useful for treating and diagnosing disorders
CC   such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's
CC   disease, ulcerative colitis), immune disorders (e.g. acquired
CC   immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes),
CC   haematopoietic disorders, neural disorders (e.g. Alzheimer's,
CC   Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis,
CC   schizophrenia), and connective disorders (e.g. osteoporosis, arthritis).
CC   ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX
SQ   Sequence 310 AA;

  Query Match           99.6%;  Score 1629;  DB 5;  Length 310;
  Best Local Similarity  99.7%;  Pred. No. 8.6e-131;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


Search completed: April 12, 2004, 09:14:45
Job time : 62 secs
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PR   30-MAR-2000; 2000WO-US008439.
PR   30-MAY-2000; 2000WO-US014941.
PR   02-JUN-2000; 2000WO-US015264.
PR   01-DEC-2000; 2000WO-US032678.
PR   25-MAY-2001; 2001US-00866034.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2002-665999/71.
DR   N-PSDB; ABS67460.
XX
PT   New human secreted and transmembrane (PRO) polypeptides, useful for
PT   treating conditions requiring PRO polypeptides, for screening PRO
PT   antagonists and agonists useful as drug candidates.
XX
PS   Claim 12; Fig 14; 125pp; English.
XX
CC   The invention relates to new human secreted and transmembrane proteins
CC   (PRO) and nucleic acids of the invention. The polypeptides can be
CC   administered therapeutically, especially by expressing encoding
CC   polynucleotides, e.g. in therapeutic compositions. They can be used to
CC   screen for PRO polypeptide antagonists and agonists useful to identify
CC   drug candidates. They can also be used to produce antibodies, useful to
CC   detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or
CC   therapeutically (e.g. as antagonists or to target and/or deliver
CC   cytotoxic agents). The polynucleotides are useful therapeutically e.g. to
CC   produce antisense sequences to inhibit polypeptide production. They can
CC   be used to produce probes and primers useful to detect or isolate
CC   sequences encoding PRO polypeptides or similar sequences e.g. variants or
CC   sequences from other species. They are also useful for gene mapping and
CC   to generate transgenic animals. ABG91355-ABG91363 represent human PRO
CC   amino acid sequences of the invention
XX
SQ   Sequence 310 AA;

  Query Match             99.6%;  Score 1629;  DB 5;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 8.6e-131;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 14
ABB84947
ID   ABB84947 standard; protein; 310 AA.
XX
AC   ABB84947;
XX
DT   16-MAY-2002  (first entry)
XX
DE   Human PRO1868 protein sequence SEQ ID NO:262.
XX
KW   Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW   vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW   gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW   angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW   age-related macular degeneration; arterial restenosis; angina;
KW   rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW   lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW   wound healing; chromosome mapping; gene mapping.
XX
OS   Homo sapiens.
XX
PN   WO200200690-A2.
XX
PD   03-JAN-2002.
XX
PF   20-JUN-2001; 2001WO-US019692.
XX
PR   23-JUN-2000; 2000US-0213637P.
PR   20-JUL-2000; 2000US-0219556P.
PR   25-JUL-2000; 2000US-0220624P.
PR   25-JUL-2000; 2000US-0220664P.
PR   28-JUL-2000; 2000WO-US020710.
PR   02-AUG-2000; 2000US-0222695P.
PR   17-AUG-2000; 2000US-00643657.
PR   23-AUG-2000; 2000WO-US023522.
PR   24-AUG-2000; 2000WO-US023328.
PR   07-SEP-2000; 2000US-0230978P.
PR   18-SEP-2000; 2000US-00664610.
PR   18-SEP-2000; 2000US-00665350.
PR   24-OCT-2000; 2000US-0242922P.
PR   08-NOV-2000; 2000US-00709238.
PR   08-NOV-2000; 2000WO-US030952.
PR   10-NOV-2000; 2000WO-US030873.
PR   01-DEC-2000; 2000WO-US032678.
PR   20-DEC-2000; 2000US-00747259.
PR   20-DEC-2000; 2000WO-US034956.
PR   22-JAN-2001; 2001US-00767609.
PR   28-FEB-2001; 2001US-00796498.
PR   28-FEB-2001; 2001WO-US006520.
PR   01-MAR-2001; 2001WO-US006666.
PR   09-MAR-2001; 2001US-00802706.
PR   14-MAR-2001; 2001US-00808689.
PR   22-MAR-2001; 2001US-00816744.
PR   05-APR-2001; 2001US-00828366.
PR   10-MAY-2001; 2001US-00854208.
PR   10-MAY-2001; 2001US-00854280.
PR   25-MAY-2001; 2001US-00866028.
PR   25-MAY-2001; 2001US-00866034.
PR   25-MAY-2001; 2001WO-US017092.
PR   30-MAY-2001; 2001US-00870574.
PR   30-MAY-2001; 2001WO-US017443.
PR   01-JUN-2001; 2001WO-US017800.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Ferrara N,  Gerber H,  Gerritsen ME,  Goddard A;
PI   Godowski PJ,  Gurney AL,  Hillan KJ,  Marsters SA,  Pan J,  Paoni NF;
PI   Stephan JF,  Watanabe CK,  Williams PM,  Wood WI,  Ye W;
XX
DR   WPI; 2002-090516/12.
DR   N-PSDB; ABL88202.
XX
PT   One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT   useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT   infarction), endothelial or angiogenic disorders in a mammal.
XX
PS   Claim 11; Fig 262; 565pp; English.
XX
```

KW systemic lupus erythematosus; systemic sclerosis; thyroiditis;
KW autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
KW psoriasis; allergic disease of the lung; graft-versus host disease;
KW tumour; gene therapy.
XX
OS Homo sapiens.
XX
PN US2002098506-A1.
XX
PD 25-JUL-2002.
XX
PF 27-DEC-2001; 2001US-00033301.
XX
PR 04-AUG-1998; 98US-0095325P.
PR 16-DEC-1998; 98US-0112851P.
PR 16-DEC-1998; 98US-0113145P.
PR 22-DEC-1998; 98US-0113511P.
PR 12-JAN-1999; 99US-0115558P.
PR 12-JAN-1999; 99US-0115565P.
PR 12-JAN-1999; 99US-0115733P.
PR 09-FEB-1999; 99US-0119341P.
PR 10-FEB-1999; 99US-0119537P.
PR 12-FEB-1999; 99US-0119965P.
PR 02-JUN-1999; 99WO-US012252.
PR 29-OCT-1999; 99US-0162506P.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 30-MAR-2000; 2000WO-US008439.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 01-DEC-2000; 2000WO-US032678.
PR 25-MAY-2001; 2001US-00866034.
XX
PA (GETH) GENENTECH INC.
XX
PI Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX
DR WPI; 2002-690475/74.
DR N-PSDB; ABS68392.
XX
PT Novel secreted and transmembrane polypeptides and polynucleotides useful
PT for diagnosis and treatment of inflammatory disorders and immune-related
PT diseases, and identifying modulators.
XX
PS Claim 12; Fig 14; 125pp; English.
XX
CC The invention relates to an isolated polypeptide having at least 80%
CC amino acid sequence identity to secreted and transmembrane polypeptides
CC PRO1800, PRO539, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434 or
CC PRO1927 and their encoding nucleic acids. Also included are vectors, host
CC cells and antibodies against PRO polypeptides. PRO proteins are useful
CC for identifying modulators of the polypeptide. PRO1868 useful for the
CC diagnosis and treatment of inflammatory and immune related diseases
CC including systemic lupus erythematosus, rheumatoid arthritis, systemic
CC sclerosis, autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus,
CC infectious hepatitis, psoriasis, allergic diseases of the lung and graft-
CC versus host disease and tumours. Pro nucleic acids are useful for
CC constructing hybridisation probes for mapping the gene that encodes that
CC PRO and for the genetic analysis of individuals with genetic disorders,
CC and for generating transgenic animals which are useful in the development
CC and screening of therapeutically useful reagents. PRO nucleic acids are
CC also useful for gene therapy, chromosome identification, and tissue
CC typing. PRO proteins are useful as molecular weight markers for protein
CC electrophoresis purposes. The anti-PRO antibodies are useful in
CC diagnostic assays for PRO, e.g. detecting its expression in specific
CC cells, tissues or serum and for affinity purification of PRO. The present
CC sequence represents a PRO protein
XX
SQ Sequence 310 AA;

Query Match 99.6%; Score 1629; DB 5; Length 310;
Best Local Similarity 99.7%; Pred. No. 8.6e-131;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 13
ABG91361
ID ABG91361 standard; protein; 310 AA.
XX
AC ABG91361;
XX
DT 29-NOV-2002 (first entry)
XX
DE Novel human secreted protein #7.
XX
KW Human; secreted protein; transmembrane protein; gene mapping; transgenic;
KW immunogenic.
XX
OS Homo sapiens.
XX
PN US2002098505-A1.
XX
PD 25-JUL-2002.
XX
PF 28-DEC-2001; 2001US-00033246.
XX
PR 04-AUG-1998; 98US-0095325P.
PR 16-DEC-1998; 98US-0112851P.
PR 16-DEC-1998; 98US-0113145P.
PR 22-DEC-1998; 98US-0113511P.
PR 12-JAN-1999; 99US-0115558P.
PR 12-JAN-1999; 99US-0115565P.
PR 12-JAN-1999; 99US-0115733P.
PR 09-FEB-1999; 99US-0119341P.
PR 10-FEB-1999; 99US-0119537P.
PR 12-FEB-1999; 99US-0119965P.
PR 02-JUN-1999; 99WO-US012252.
PR 29-OCT-1999; 99US-0162506P.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.

PR 23-JUL-1999; 99US-0145220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX
PS Claim 11; Page 557-558; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations
XX
SQ Sequence 310 AA;

Query Match 99.6%; Score 1629; DB 4; Length 310;
Best Local Similarity 99.7%; Pred. No. 8.6e-131;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 11
AAB80409
ID AAB80409 standard; protein; 310 AA.
XX
AC AAB80409;
XX
DT 24-APR-2001 (first entry)
XX
DE Secreted protein encoded by gene #39.
XX
KW Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW cerebrovascular; infection; food.
XX
OS Homo sapiens.
XX
PN WO200107459-A1.
XX

PD 01-FEB-2001.
XX
PF 20-JUL-2000; 2000WO-US019735.
XX
PR 23-JUL-1999; 99US-0145220P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Ebner R, Duan RD, Ni J, Soppet DR, Moore PA;
PI Shi Y, Lafleur DW, Olsen HS, Birse CE, Komatsoulis GA;
XX
DR WPI; 2001-123261/13.
XX
PT New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT preventing and treating e.g. autoimmune, hyperproliferative,
PT cardiovascular, and ocular diseases or disorders and microorganism
PT infections.
XX
PS Claim 11; Page 559-560; 601pp; English.
XX
CC The present invention relates to 29 human secreted proteins. The
CC invention is used to prevent autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. Also used in food
CC preparations
XX
SQ Sequence 310 AA;

Query Match 99.6%; Score 1629; DB 4; Length 310;
Best Local Similarity 99.7%; Pred. No. 8.6e-131;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 12
ABG92709
ID ABG92709 standard; protein; 310 AA.
XX
AC ABG92709;
XX
DT 18-NOV-2002 (first entry)
XX
DE Human secreted protein PRO1868.
XX
KW Human; secreted and transmembrane protein; PRO1800; PRO539; PRO982;
KW PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927;
KW inflammatory disorder; immune related disease; rheumatoid arthritis;

```
CC   polypeptides, and to detect the presence of mammalian lung, colon,
CC   breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC   polypeptide expression in a cell sample to that in a control sample. Some
CC   of the 275 sequences are also useful to stimulate the release of tumour
CC   necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC   differentiation of chondrocytes, the proliferation or gene expression in
CC   pericyte cells, the release of proteoglycans from cartilage, the
CC   proliferation of inner ear utricular supporting cells or of T-
CC   lymphocytes, the release of a cytokine from peripheral blood monocytes
CC   (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC   polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC   muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC   VIIA. The PRO polypeptides can be used in assays to identify molecules
CC   involved in binding interactions. The polynucleotides encoding PRO
CC   polypeptides can be used to generate probes, antisense RNA/DNA,
CC   transgenic or knock out animals and can be used in gene therapy
XX
SQ   Sequence 310 AA;

  Query Match             99.6%;  Score 1629;  DB 4;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 8.6e-131;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 9
AAB80383
ID   AAB80383 standard; protein; 310 AA.
XX
AC   AAB80383;
XX
DT   24-APR-2001  (first entry)
XX
DE   Secreted protein encoded by gene #13.
XX
KW   Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW   cerebrovascular; infection; food.
XX
OS   Homo sapiens.
XX
PN   WO200107459-A1.
XX
PD   01-FEB-2001.
XX
PF   20-JUL-2000; 2000WO-US019735.
XX
PR   23-JUL-1999;   99US-0145220P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM,  Ebner R,  Duan RD,  Ni J,  Soppet DR,  Moore PA;
PI   Shi Y,  Lafleur DW,  Olsen HS,  Birse CE,  Komatsoulis GA;
XX
DR   WPI; 2001-123261/13.
XX
PT   New isolated nucleic acid encoding 29 secreted proteins, for diagnosing,
PT   preventing and treating e.g. autoimmune, hyperproliferative,
PT   cardiovascular, and ocular diseases or disorders and microorganism
PT   infections.
XX
PS   Claim 11; Page 538-539; 601pp; English.
XX
CC   The present invention relates to 29 human secreted proteins. The
CC   invention is used to prevent autoimmune diseases e.g. rheumatoid
CC   arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC   liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC   disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC   e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC   fungi and ocular disorders e.g. corneal infection. Also used in food
CC   preparations
XX
SQ   Sequence 310 AA;

  Query Match             99.6%;  Score 1629;  DB 4;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 8.6e-131;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 10
AAB80408
ID   AAB80408 standard; protein; 310 AA.
XX
AC   AAB80408;
XX
DT   24-APR-2001  (first entry)
XX
DE   Secreted protein encoded by gene #38.
XX
KW   Secreted protein; human; autoimmune; hyperproliferation; cardiovascular;
KW   cerebrovascular; infection; food.
XX
OS   Homo sapiens.
XX
PN   WO200107459-A1.
XX
PD   01-FEB-2001.
XX
PF   20-JUL-2000; 2000WO-US019735.
XX
```

PF 07-JUL-2000; 2000EP-00114089.
XX
PR 08-JUL-1999; 99JP-00194486.
PR 11-JAN-2000; 2000JP-00118774.
PR 02-MAY-2000; 2000JP-00183765.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR WPI; 2001-524255/58.
DR N-PSDB; AAK94243.
XX
PT 830 Primers useful for synthesizing full length cDNA clones and their use
PT in genetic manipulation.
XX
PS Claim 8; SEQ ID NO 2845; 1380pp + Sequence Listing; English.
XX
CC The invention relates to primers for synthesising full length cDNA
CC clones. 830 cDNA molecules encoding a human protein have been isolated
CC and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC been determined. Primers for synthesising the full length cDNA are useful
CC for clarifying the function of the protein encoded by the cDNA. The full
CC length clones were obtained by construction of full length enriched cDNA
CC libraries that were synthesised by the oligo-capping method. The primers
CC enable the production of the full length cDNA easily without any special
CC methods. The present sequence is a polypeptide encoded by a full length
CC human cDNA of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in CD-ROM
CC format directly from EPO
XX
SQ Sequence 310 AA;

Query Match 99.6%; Score 1629; DB 4; Length 310;
Best Local Similarity 99.7%; Pred. No. 8.6e-131;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 8
AAU12440
ID AAU12440 standard; protein; 310 AA.
XX
AC AAU12440;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO1868 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21512.
XX
PT Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 538; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO

```
XX
PS   Claim 1; Fig 124; 393pp; English.
XX
CC   The present sequence is one of sixty one novel secreted and transmembrane
CC   PRO polypeptides. The PRO polypeptides are useful for treating skin
CC   diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma),
CC   gastrointestinal disorders (e.g. enterocolitis), neurodegenerative
CC   diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair,
CC   cardiovascular disorders (e.g. endometrial bleeding angiogenesis,
CC   ischaemias such as coronary ischaemia, atherosclerosis), inflammatory
CC   disorders (e.g. asthma, rheumatoid arthritis, multiple sclerosis),
CC   infertility, AIDS and diabetes and retinal disorders such as retinitis
CC   pigmentosum. The PRO nucleic acids have applications in molecular
CC   biology, including use as hybridization probes, and in chromosome and
CC   gene mapping
XX
SQ   Sequence 310 AA;

  Query Match             99.6%;  Score 1629;  DB 4;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 8.6e-131;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 6
AAM93905
ID   AAM93905 standard; protein; 310 AA.
XX
AC   AAM93905;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide, SEQ ID NO: 4051.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-00114089.
XX
PR   08-JUL-1999;   99JP-00194486.
PR   11-JAN-2000; 2000JP-00118774.
PR   02-MAY-2000; 2000JP-00183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
PI   Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX
DR   WPI; 2001-524255/58.
DR   N-PSDB; AAK94867.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their use
PT   in genetic manipulation.
XX
PS   Claim 8; SEQ ID NO 4051; 1380pp + Sequence Listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been isolated
CC   and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have
CC   been determined. Primers for synthesising the full length cDNA are useful
CC   for clarifying the function of the protein encoded by the cDNA. The full
CC   length clones were obtained by construction of full length enriched cDNA
CC   libraries that were synthesised by the oligo-capping method. The primers
CC   enable the production of the full length cDNA easily without any special
CC   methods. The present sequence is a polypeptide encoded by a full length
CC   human cDNA of the invention. Note: The sequence data for this patent did
CC   not form part of the printed specification, but was obtained in CD-ROM
CC   format directly from EPO
XX
SQ   Sequence 310 AA;

  Query Match             99.6%;  Score 1629;  DB 4;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 8.6e-131;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 7
AAM93323
ID   AAM93323 standard; protein; 310 AA.
XX
AC   AAM93323;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide, SEQ ID NO: 2845.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
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Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 4
AAB27276
ID AAB27276 standard; protein; 310 AA.
XX
AC AAB27276;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human confluency regulated adhesion molecule 1 #2.
XX
KW Immunoglobulin superfamily; Ig Sf; vascular adhesion molecule;
KW inflammation; cancer; wound; angiogenesis; human;
KW confluency regulated adhesion molecule 1; CRAM-1; JAM-2.
XX
OS Homo sapiens.
XX
PN WO200053749-A2.
XX
PD 14-SEP-2000.
XX
PF 13-MAR-2000; 2000WO-EP002219.
XX
PR 11-MAR-1999; 99EP-00200746.
XX
PA (RMFD-) RMF DICTAGENE SA.
XX
PI Imhof BA, Aurrand-Lions M;
XX
DR WPI; 2000-587436/55.
DR N-PSDB; AAA95306.
XX
PT Isolated human Confluency Regulated Adhesion Molecule 1 or 2 (CRAM-1 or
PT CRAM-2) polypeptide, useful for treatment of tumors, inflammation
PT reactions and modulating vascular permeability.
XX
PS Claim 2; Fig 6; 59pp; English.
XX
CC The present sequence is the human confluency regulated adhesion molecule
CC 1 (CRAM-1, also known as JAM-2). CRAM-1 is one of the vascular adhesion
CC proteins of the immunoglobulin superfamily (Ig Sf). The CRAM-1 protein
CC and coding sequence can be used in the treatment of cancer, inflammation,
CC to modulate cell-cell interactions and angiogenesis, and in the
CC modulation of wound healing
XX
SQ Sequence 310 AA;

Query Match 99.6%; Score 1629; DB 3; Length 310;
Best Local Similarity 99.7%; Pred. No. 8.6e-131;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

RESULT 5
AAB80272
ID AAB80272 standard; protein; 310 AA.
XX
AC AAB80272;
XX
DT 24-APR-2001 (first entry)
XX
DE Human PRO1868 protein.
XX
KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
KW antiparkinsonian nootropic; neuroprotective; vulnerary; cardiant;
KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
KW antiarthritic; antiinfertility; antidiabetic; antiviral; diabetes;
KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
KW ischaemia; inflammation.
XX
OS Homo sapiens.
XX
PN WO200104311-A1.
XX
PD 18-JAN-2001.
XX
PF 22-FEB-2000; 2000WO-US004414.
XX
PR 07-JUL-1999; 99US-0143048P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;
XX
DR WPI; 2001-081051/09.
DR N-PSDB; AAF72433.
XX
PT Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT disease).

```
Qy          61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy         121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy         181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
               |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy         241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy         301 DFRHKSSFVI 310
               ||||||||||
Db         301 DFRHKSSFVI 310
```

RESULT 3
AAB33457
ID AAB33457 standard; protein; 310 AA.
XX
AC AAB33457;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human PRO1868 protein UNQ859 SEQ ID NO:193.
XX
KW Human; immune related disease; diagnosis; antiinflammatory; cardiant;
KW dermatological; antiarthritic; antirheumatic; immunosuppressive;
KW haemostatic; antithyroid; antidiabetic; nootropic; neuroprotective;
KW antianaemic; hepatotropic; virucide; antipsoriatic; antiallergic;
KW antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
KW autoimmune thrombocytopaenia; immune-mediated renal disease;
KW demyelinating disease; hepatobiliary disease; Whipple's disease;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW autoimmune disease; immune-mediated skin disease; allergic disease;
KW immunological disease; transplantation associated disease;
KW graft rejection; graft-versus-host-disease.
XX
OS Homo sapiens.
XX
PN WO200053758-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-US005841.
XX
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-MAR-1999; 99US-0123957P.
PR 23-MAR-1999; 99US-0125775P.
PR 12-APR-1999; 99US-0128849P.
PR 20-APR-1999; 99WO-US008615.
PR 28-APR-1999; 99US-0131445P.
PR 04-MAY-1999; 99US-0132371P.
PR 14-MAY-1999; 99US-0134287P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-OCT-1999; 99US-0162506P.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
XX
DR WPI; 2000-572271/53.
DR N-PSDB; AAC58622.
XX
PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of
PT immune related disorders, e.g. systemic lupus erythematosis, rheumatoid
PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
XX
PS Claim 33; Fig 88; 309pp; English.
XX
CC The present invention describes sixty four human PRO proteins which can
CC be used in the treatment of immune related diseases. The human PRO
CC proteins, anti-PRO antibodies, agonists and antagonists are useful for
CC treating and diagnosing immune related disorders. The disorders are
CC selected from systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
CC immune-mediated renal disease, demyelinating diseases of the central and
CC peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
CC disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune
CC or immune-mediated skin diseases, allergic diseases, immunological
CC diseases of the lung, and transplantation associated diseases including
CC graft rejection and graft-versus-host-disease. AAC58397 to AAC58578
CC represent PCR primers and hybridisation probes used in the isolation of
CC human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33477
CC represent human PRO polynucleotide and protein sequences given in the
CC exemplification of the present invention
XX
SQ Sequence 310 AA;

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  Query Match             99.6%;  Score 1629;  DB 3;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 8.6e-131;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy           1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
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Qy          61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
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Qy         121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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XX
PS   Claim 1; Page 82-83; 105pp; English.
XX
CC   The present sequence is the human immunoglobulin superfamily protein
CC   IGFAM-6. Its gene was isolated from a cDNA library of leg tissue. It is
CC   expressed in reproductive, nervous and cardiovascular tissue, where
CC   cancer and inflammation are common. The gene, protein, its antibodies,
CC   agonists and antagonists are suitable for diagnosing and treating many
CC   diseases, including cancer, immune system disorders (such as
CC   inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma,
CC   atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus,
CC   emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis,
CC   rheumatoid arthritis, scleroderma, systemic lupus erythematosus and
CC   ulcerative colitis), complications of cancer, haemodialysis and
CC   extracorporeal circulation, trauma and haematopoietic cancer (such as
CC   leukaemia) and infections caused by bacteria, viruses, fungi or parasites
XX
SQ   Sequence 310 AA;

  Query Match             100.0%;  Score 1635;  DB 3;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 2.7e-131;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
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Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
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Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 2
AAY96735
ID   AAY96735 standard; protein; 310 AA.
XX
AC   AAY96735;
XX
DT   26-SEP-2000  (first entry)
XX
DE   PRO1868, an A33 antigen homologue.
XX
KW   PRO1868; A33 antigen; secreted protein; transmembrane protein;
KW   anti-inflammatory; cytostatic; recombinant production; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .30
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FT                   /note= "Tyrosine kinase phosphorylation site"
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FT                   /note= "N-glycosylation site"
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FT   Modified-site   107. .110
FT                   /note= "cAMP- and cGMP-dependent protein kinase
FT                   phosphorylation site"
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FT                   /note= "N-myristoylation site"
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FT                   /note= "N-myristoylation site"
FT   Modified-site   262. .267
FT                   /note= "N-myristoylation site"
FT   Modified-site   296. .299
FT                   /note= "Casein kinase II phosphorylation site"
XX
PN   WO200036102-A2.
XX
PD   22-JUN-2000.
XX
PF   01-DEC-1999;   99WO-US028634.
XX
PR   16-DEC-1998;   98US-0112851P.
PR   16-DEC-1998;   98US-0113145P.
PR   22-DEC-1998;   98US-0113511P.
PR   12-JAN-1999;   99US-0115558P.
PR   12-JAN-1999;   99US-0115565P.
PR   12-JAN-1999;   99US-0115733P.
PR   09-FEB-1999;   99US-0119341P.
PR   10-FEB-1999;   99US-0119537P.
PR   12-FEB-1999;   99US-0119965P.
PR   02-JUN-1999;   99WO-US012252.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Botstein D,  Desnoyers L,  Ferrara N,  Fong S,  Gao W,  Goddard A;
PI   Gurney AL,  Pan J,  Roy MA,  Stewart TA,  Tumas D,  Watanabe CK;
PI   Wood WI;
XX
DR   WPI; 2000-431586/37.
DR   N-PSDB; AAA51265.
XX
PT   Isolated nucleic acid molecule encodes a PRO polypeptide which is a
PT   transmembrane polypeptide.
XX
PS   Claim 1; Fig 14; 154pp; English.
XX
CC   This is PRO1868, a putative homologue of A33 antigen, a known colorectal
CC   cancer-associated marker. The invention concerns novel secreted and
CC   transmembrane proteins, designated PRO polypeptides. The cDNA and gene
CC   sequences are useful in the recombinant production of PRO polypeptides,
CC   as a hybridization probe to screen libraries to isolate cDNAs with
CC   sequence identity to PRO polypeptides or to map the gene encoding the PRO
CC   polypeptides and analyzing genetic disorders. The cDNA/gene can also be
CC   used to produce transgenic animals useful for the development and
CC   screening of therapeutically useful reagents. They can also be used in
CC   gene therapy, e.g. to replace a defective gene
XX
SQ   Sequence 310 AA;

  Query Match             99.6%;  Score 1629;  DB 3;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 8.6e-131;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:08:18 ; Search time 59 Seconds
(without alignments)
1484.572 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 1635
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1629	99.6	310	3	AAB33457	Aab33457 Human PRO
4	1629	99.6	310	3	AAB27276	Aab27276 Human con
5	1629	99.6	310	4	AAB80272	Aab80272 Human PRO
6	1629	99.6	310	4	AAM93905	Aam93905 Human pol
7	1629	99.6	310	4	AAM93323	Aam93323 Human pol
8	1629	99.6	310	4	AAU12440	Aau12440 Human PRO
9	1629	99.6	310	4	AAB80383	Aab80383 Secreted
10	1629	99.6	310	4	AAB80408	Aab80408 Secreted
11	1629	99.6	310	4	AAB80409	Aab80409 Secreted
12	1629	99.6	310	5	ABG92709	Abg92709 Human sec
13	1629	99.6	310	5	ABG91361	Abg91361 Novel hum
14	1629	99.6	310	5	ABB84947	Abb84947 Human PRO
15	1629	99.6	310	5	ABG65297	Abg65297 Human alb
16	1629	99.6	310	5	ABG65296	Abg65296 Human alb
17	1629	99.6	310	5	ABG65298	Abg65298 Human alb
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19	1629	99.6	310	5	ABB95553	Abb95553 Human ang
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22	1629	99.6	310	6	ABU80867	Abu80867 Human sec
23	1629	99.6	310	6	ABO17884	Abo17884 Novel hum
24	1629	99.6	310	6	ABU71505	Abu71505 Human PRO
25	1629	99.6	310	6	ADA57610	Ada57610 Human sec
26	1629	99.6	310	6	ADA57611	Ada57611 Human sec
27	1629	99.6	310	6	ADA57309	Ada57309 Human sec
28	1629	99.6	310	6	ABP71277	Abp71277 Human jun
29	1629	99.6	310	6	ABU81138	Abu81138 Human PRO
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35	1629	99.6	310	6	ABG73314	Abg73314 Human PRO
36	1629	99.6	310	6	ABU59919	Abu59919 Novel sec
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ALIGNMENTS

RESULT 1
AAY96294
ID AAY96294 standard; protein; 310 AA.
XX
AC AAY96294;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human IGFAM-6 immunoglobulin.
XX
KW Human; immunoglobulin; IGFAM-6; IGFAM; immune disorder; cancer;
KW infection; inflammation; haematopoiesis; AIDS; allergy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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XX
PN WO200029583-A2.
XX
PD 25-MAY-2000.
XX
PF 19-NOV-1999; 99WO-US027566.
XX
PR 19-NOV-1998; 98US-00195853.
PR 22-DEC-1998; 98US-0113635P.
PR 07-APR-1999; 99US-0128194P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
PI Lu DAM, Lal P, Hillman JL, Yang J;
XX
DR WPI; 2000-387796/33.
DR N-PSDB; AAA27386.
XX
PT Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT protein is useful for preventing and treating disorders associated with
PT altered levels of the protein such as cancer, immune system disorders.

; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,786
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-904-786-423

Query Match 99.6%; Score 1629; DB 10; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
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Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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Job time : 46 secs

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RESULT 14
US-09-904-820-423
; Sequence 423, Application US/09904820
; Publication No. US20030036094A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,820
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
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;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
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; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-820-423

  Query Match             99.6%;  Score 1629;  DB 10;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 9.6e-133;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
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Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 15
US-09-904-786-423
; Sequence 423, Application US/09904786
; Publication No. US20030039969A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
```

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;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-904-859-423

  Query Match             99.6%;  Score 1629;  DB 10;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 9.6e-133;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 13
US-09-909-204-423
; Sequence 423, Application US/09909204
; Publication No. US20030036061A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Klein, Ivan J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/909,204
;  CURRENT FILING DATE:  2001-07-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-909-204-423

  Query Match             99.6%;  Score 1629;  DB 10;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 9.6e-133;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
```

```
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,942
;  CURRENT FILING DATE:  2002-01-22
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-907-942-423

  Query Match            99.6%;  Score 1629;  DB 10;  Length 310;
  Best Local Similarity  99.7%;  Pred. No. 9.6e-133;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDPFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 12
US-09-904-859-423
; Sequence 423, Application US/09904859
; Publication No. US20030036060A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/904,859
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
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```
Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
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Db        301 DFRHKSSFVI 310
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RESULT 10
US-09-907-613-423
; Sequence 423, Application US/09907613
; Publication No. US20030027145A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,613
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-613-423

Query Match 99.6%; Score 1629; DB 10; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
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Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
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Db        301 DFRHKSSFVI 310
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RESULT 11
US-09-907-942-423
; Sequence 423, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

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;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-906-742-423

  Query Match             99.6%;  Score 1629;  DB 10;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 9.6e-133;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
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Db        301 DFRHKSSFVI 310


RESULT 9
US-09-906-838-423
; Sequence 423, Application US/09906838
; Publication No. US20030027143A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/906,838
;  CURRENT FILING DATE:  2001-07-16
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-906-838-423

  Query Match             99.6%;  Score 1629;  DB 10;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 9.6e-133;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien

US-09-904-011-423

Query Match 99.6%; Score 1629; DB 10; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
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Db        301 DFRHKSSFVI 310
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RESULT 8
US-09-906-742-423
; Sequence 423, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698

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;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-907-824-423

  Query Match             99.6%;  Score 1629;  DB 9;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 9.6e-133;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
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Db        301 DFRHKSSFVI 310


RESULT 6
US-09-907-841-423
; Sequence 423, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,841
;  CURRENT FILING DATE:  2001-11-20
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-907-841-423

  Query Match             99.6%;  Score 1629;  DB 9;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 9.6e-133;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 7
US-09-904-011-423
; Sequence 423, Application US/09904011
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;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,853
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: US/09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-902-853-423

  Query Match             99.6%;  Score 1629;  DB 9;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 9.6e-133;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
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Qy        301 DFRHKSSFVI 310
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RESULT 5
US-09-907-824-423
; Sequence 423, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,824
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: 09/665,350
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
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Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
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Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
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Db        301 DFRHKSSFVI 310
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RESULT 3
US-09-905-291A-423
; Sequence 423, Application US/09905291A
; Patent No. US20020160374A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,291A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-905-291A-423

Query Match 99.6%; Score 1629; DB 9; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
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Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
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Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
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Db        301 DFRHKSSFVI 310
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RESULT 4
US-09-902-853-423
; Sequence 423, Application US/09902853
; Publication No. US20020192659A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter

; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-320-423

Query Match 99.6%; Score 1629; DB 9; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
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Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
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Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
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Qy        301 DFRHKSSFVI 310
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RESULT 2
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; Sequence 423, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,088B
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
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; PRIOR APPLICATION NUMBER: PCT/US99/21090
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-909-088B-423

Query Match 99.6%; Score 1629; DB 9; Length 310;
Best Local Similarity 99.7%; Pred. No. 9.6e-133;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:16:19 ; Search time 46 Seconds
(without alignments)
1771.973 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 1635
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1629	99.6	310	9	US-09-909-320-423	Sequence 423, App
2	1629	99.6	310	9	US-09-909-088B-423	Sequence 423, App
3	1629	99.6	310	9	US-09-905-291A-423	Sequence 423, App
4	1629	99.6	310	9	US-09-902-853-423	Sequence 423, App
5	1629	99.6	310	9	US-09-907-824-423	Sequence 423, App
6	1629	99.6	310	9	US-09-907-841-423	Sequence 423, App
7	1629	99.6	310	10	US-09-904-011-423	Sequence 423, App
8	1629	99.6	310	10	US-09-906-742-423	Sequence 423, App
9	1629	99.6	310	10	US-09-906-838-423	Sequence 423, App
10	1629	99.6	310	10	US-09-907-613-423	Sequence 423, App
11	1629	99.6	310	10	US-09-907-942-423	Sequence 423, App
12	1629	99.6	310	10	US-09-904-859-423	Sequence 423, App
13	1629	99.6	310	10	US-09-909-204-423	Sequence 423, App
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16	1629	99.6	310	10	US-09-906-646-423	Sequence 423, App
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18	1629	99.6	310	10	US-09-903-786-423	Sequence 423, App
19	1629	99.6	310	10	US-09-902-903-423	Sequence 423, App
20	1629	99.6	310	10	US-09-903-749A-423	Sequence 423, App
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23	1629	99.6	310	10	US-09-902-736-423	Sequence 423, App
24	1629	99.6	310	10	US-09-907-794-423	Sequence 423, App
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26	1629	99.6	310	10	US-09-904-462-423	Sequence 423, App
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28	1629	99.6	310	10	US-09-902-692-423	Sequence 423, App
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31	1629	99.6	310	10	US-09-909-064-423	Sequence 423, App
32	1629	99.6	310	10	US-09-904-553-423	Sequence 423, App
33	1629	99.6	310	10	US-09-905-381-423	Sequence 423, App
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35	1629	99.6	310	10	US-09-907-575-423	Sequence 423, App
36	1629	99.6	310	10	US-09-905-075-423	Sequence 423, App
37	1629	99.6	310	10	US-09-902-759-423	Sequence 423, App
38	1629	99.6	310	10	US-09-902-634-423	Sequence 423, App
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41	1629	99.6	310	10	US-09-902-615-423	Sequence 423, App
42	1629	99.6	310	10	US-09-903-925-423	Sequence 423, App
43	1629	99.6	310	10	US-09-906-760A-423	Sequence 423, App
44	1629	99.6	310	10	US-09-903-823-423	Sequence 423, App
45	1629	99.6	310	10	US-09-907-652-423	Sequence 423, App

ALIGNMENTS

RESULT 1
US-09-909-320-423
; Sequence 423, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,320
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048

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Qy        303 RHKSSFVI 310
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Db        292 KQTSSFLV 299


RESULT 15
US-09-907-794A-119
; Sequence 119, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,794A
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 119
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-907-794A-119

  Query Match           25.6%;  Score 419;  DB 4;  Length 299;
  Best Local Similarity  32.8%;  Pred. No. 8.4e-35;
  Matches  101;  Conservative   47;  Mismatches  138;  Indels   22;  Gaps    7;

Qy          8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
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Db          9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              |  | :  |  | ::|||       |   |  | :   :||| |:  | | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |: ::| | | |  |  :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
              | |||  ||  || |||  :   |:|:| | | |  |:         ||  : |:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
              |||  | :| ::  ||  || ||:|   |:   |    |  |            ||:|
Db        241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy        303 RHKSSFVI 310
              :  |||::
Db        292 KQTSSFLV 299


Search completed: April 12, 2004, 09:20:35
Job time : 23 secs
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;  FILE REFERENCE:  P1216R1(US)
;  CURRENT APPLICATION NUMBER: US/09/254,465A
;  CURRENT FILING DATE:  1999-03-05
;  PRIOR APPLICATION NUMBER:  PCT/US98/24855
;  PRIOR FILING DATE:  1998-11-20
;  PRIOR APPLICATION NUMBER:  US 60/066,364
;  PRIOR FILING DATE:  1997-11-21
;  PRIOR APPLICATION NUMBER:  US 60/078,936
;  PRIOR FILING DATE:  1998-03-20
;  PRIOR APPLICATION NUMBER:  PCT/US98/19437
;  PRIOR FILING DATE:  1998-09-17
;  NUMBER OF SEQ ID NOS:  30
; SEQ ID NO 1
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-254-465A-1

  Query Match             25.6%;  Score 419;  DB 4;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 8.4e-35;
  Matches  101;  Conservative   47;  Mismatches  138;  Indels   22;  Gaps    7;

Qy          8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
              |  ||      | | :|     :|:| : ||     : |   |:|||    |  | ||:||
Db          9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              |  | : |  | ::|||       |   |  | :   :||| |:  | | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |: ::| | | |  |   :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
              | |||  ||  || |||  :   |:|:| | | |  |:        ||  : :|:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
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Db        241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy        303 RHKSSFVI 310
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Db        292 KQTSSFLV 299


RESULT 13
US-09-312-283C-189
; Sequence 189, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT:  Strachan, Lorna
;  APPLICANT:  Sleeman, Matthew
;  APPLICANT:  Onrust, Rene
;  APPLICANT:  Murison, James G.
;  APPLICANT:  Kumble, Krishanand D.
;  TITLE OF INVENTION: Compositions Isolated from Skin Cells
;  TITLE OF INVENTION:  and Methods for Their Use
;  FILE REFERENCE: 11000.1011c2
;  CURRENT APPLICATION NUMBER: US/09/312,283C
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS: 425
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 189
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-312-283C-189

  Query Match             25.6%;  Score 419;  DB 4;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 8.4e-35;
  Matches  101;  Conservative   47;  Mismatches  138;  Indels   22;  Gaps    7;

Qy          8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
              |  ||      | | :|     :|:| : ||     : |   |:|||    |  | ||:||
Db          9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              |  | : |  | ::|||       |   |  | :   :||| |:  | | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |: ::| | | |  |   :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
              | |||  ||  || |||  :   |:|:| | | |  |:        ||  : :|:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
              ||| | :| ::  ||  || ||:|   |:   |    | |             ||:|
Db        241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy        303 RHKSSFVI 310
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Db        292 KQTSSFLV 299


RESULT 14
US-09-312-283C-331
; Sequence 331, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT:  Strachan, Lorna
;  APPLICANT:  Sleeman, Matthew
;  APPLICANT:  Onrust, Rene
;  APPLICANT:  Murison, James G.
;  APPLICANT:  Kumble, Krishanand D.
;  TITLE OF INVENTION: Compositions Isolated from Skin Cells
;  TITLE OF INVENTION:  and Methods for Their Use
;  FILE REFERENCE: 11000.1011c2
;  CURRENT APPLICATION NUMBER: US/09/312,283C
;  CURRENT FILING DATE:  1999-05-14
;  NUMBER OF SEQ ID NOS: 425
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 331
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Mouse
US-09-312-283C-331

  Query Match             25.6%;  Score 419;  DB 4;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 8.4e-35;
  Matches  101;  Conservative   47;  Mismatches  138;  Indels   22;  Gaps    7;

Qy          8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
              |  ||      | | :|     :|:| : ||     : |   |:|||    |  | ||:||
Db          9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy         68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
              |  | : |  | ::|||       |   |  | :   :||| |:  | | :|:
Db         63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy        128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
              |: ::| | | |  |   :| :  :|  | | | | :| |   |:|::: : :||: ::
Db        121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy        188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
              | |||  ||  || |||  :   |:|:| | | |  |:        ||  : :|:| |:
Db        181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy        247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
              ||| | :| ::  ||  || ||:|   |:   |    | |             ||:|
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;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-254-465A-10

  Query Match             27.5%;  Score 449.5;  DB 4;  Length 300;
  Best Local Similarity   35.2%;  Pred. No. 6.1e-38;
  Matches  105;  Conservative   56;  Mismatches  122;  Indels   15;  Gaps    7;

Qy          20 LLLLFRGCLIGAV-----NLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEWKKIQDEQ 74
               || ||   ::|::     :: ::      | | ||::|:|  | |  | ||:||| :|
Db          11 LLFLFTSMILGSLVQGKGSVYTAQSDVQVPENESIKLTC--TYSGFSSPRVEWKFVQGST 68

Qy          75 TTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEIDEIVIELT 134
               |  | ::::|    | |      : :   :|||:|:  | | :|:    :   |: | ||
Db          69 TALVCYNSQITAPYADRV-TFSSSGITFSSVTRKDNGEYTC-MVSEEGGQNYGEVSIHLT 126

Qy         135 VQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPT-DSRANPRFRNS 193
               | | |   |   || :| :|  | | | | :| |    |||::: : : | |::    | ||
Db         127 VLVPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNS 186

Qy         194 SSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSA-RCEEQEMEVYDLNIGGIIGGVLVV 252
               |  :: ::| |:|  |    |||:||| | |  |:| | |    |:  :||:|||:  |||
Db         187 SFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGGIVAAVLVT 246

Qy         253 LAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI 310
               | :| |:  |:  || ||||   |:          |||     :   |  ||:|:  |||::
Db         247 LILLGLLIFGVWFAYSRGYFETTKKG----TAPGKKVIYSQPSTRSEGEFKQTSSFLV 300


RESULT 10
US-09-188-930-331
; Sequence 331, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
;  APPLICANT: Watson, James D.
;  APPLICANT: Strachan, Lorna
;  APPLICANT: Sleeman, Matthew
;  APPLICANT: Onrust, Rene
;  APPLICANT: Murison, James Greg
;  TITLE OF INVENTION: Compositions Isolated From Skin Cells
;  TITLE OF INVENTION: and Methods For Their Use
;  FILE REFERENCE: 11000.1011c1
;  CURRENT APPLICATION NUMBER: US/09/188,930A
;  CURRENT FILING DATE: 1998-11-09
;  NUMBER OF SEQ ID NOS: 348
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 331
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: Human
US-09-188-930-331

  Query Match             25.6%;  Score 419;  DB 3;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 8.4e-35;
  Matches  101;  Conservative   47;  Mismatches  138;  Indels   22;  Gaps    7;

Qy           8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
               |  ||      | | :|     :|:| : ||      : |    |:|||    |  | ||:||
Db           9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy          68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
               |  | : |  | ::|||       |   |  | :   :||| |:  | | :|:
Db          63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy         128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
               |: ::| | | |   :| :  :|  | | | | :| |    |:|::: : :||: ::
Db         121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy         188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
               | |||  ||  || |||  :   |:|:| | | |  |:          ||  : |:| |:
Db         181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy         247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
               |||  | :| ::  ||  || ||:|   |:   |  |  |                ||:|
Db         241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy         303 RHKSSFVI 310
               :  |||::
Db         292 KQTSSFLV 299


RESULT 11
US-09-462-270-2
; Sequence 2, Application US/09462270
; Patent No. 6358707
; GENERAL INFORMATION:
;  APPLICANT:  SmithKline Beecham Corporation
;  TITLE OF INVENTION:  Human F11 Antigen: A Cell Surface
;  TITLE OF INVENTION:  Receptor   Involved in Platelet Aggregation
;  FILE REFERENCE:  GH-70150US
;  CURRENT APPLICATION NUMBER: US/09/462,270
;  CURRENT FILING DATE:  2000-01-05
;  PRIOR APPLICATION NUMBER:  60/052,186
;  PRIOR FILING DATE:  1997-07-10
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 299
;   TYPE: PRT
;   ORGANISM: HOMO SAPIENS
US-09-462-270-2

  Query Match             25.6%;  Score 419;  DB 4;  Length 299;
  Best Local Similarity   32.8%;  Pred. No. 8.4e-35;
  Matches  101;  Conservative   47;  Mismatches  138;  Indels   22;  Gaps    7;

Qy           8 RLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSDPRIEW 67
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Db           9 RKLLCL----FILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAY--SGFSSPRVEW 62

Qy          68 KKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRKEID 127
               |  | : |  | ::|||       |   |  | :   :||| |:  | | :|:
Db          63 KFDQGDTTRLVCYNNKITASYEDRVTFL-PTGITFKSVTREDTGTYTC-MVSEEGGNSYG 120

Qy         128 EIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRAN 187
               |: ::| | | |   :| :  :|  | | | | :| |    |:|::: : :||: ::
Db         121 EVKVKLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKST 180

Qy         188 PRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQ-EMEVYDLNIGGII 246
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Db         181 RAFSNSSYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIV 240

Qy         247 GGVLVVLAVLALITLGICCAYRRGYFINNKQDGES----YKNPGKPDGVNYIRTDEEGDF 302
               |||  | :| ::  ||  || ||:|   |:   |  |  |                ||:|
Db         241 AAVLVTLILLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPS---------ARSEGEF 291

Qy         303 RHKSSFVI 310
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RESULT 12
US-09-254-465A-1
; Sequence 1, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
;  APPLICANT:  Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi J.
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION:  COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
;  TITLE OF INVENTION:  OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
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Db          51 -KTPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107

Qy         114 RCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172

Db         108 RCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

Qy         173 WYRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232

Db         168 WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227

Qy         233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYF 272

Db         228 KRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF 267


RESULT 8
US-09-902-775A-64
; Sequence 64, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,775A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-902-775A-64

  Query Match             27.9%;  Score 456.5;  DB 4;  Length 312;
  Best Local Similarity   37.1%;  Pred. No. 1.2e-38;
  Matches  104;  Conservative   51;  Mismatches  104;  Indels   21;  Gaps    7;

Qy           1 MALRRPPRLRLCARLPDFFLLLLFRGCLIG-----AVNLKSSNRTPVVQ--EFESVELSC 53

Db           1 MARRSRHRL----------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC 50

Qy          54 IITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALY 113

Db          51 -KTPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107

Qy         114 RCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172

Db         108 RCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

Qy         173 WYRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232

Db         168 WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227

Qy         233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYF 272

Db         228 KRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF 267


RESULT 9
US-09-254-465A-10
; Sequence 10, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
;  APPLICANT:  Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi J.
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION:  COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
;  TITLE OF INVENTION:  OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
;  FILE REFERENCE:  P1216R1(US)
;  CURRENT APPLICATION NUMBER: US/09/254,465A
;  CURRENT FILING DATE:  1999-03-05
;  PRIOR APPLICATION NUMBER:  PCT/US98/24855
;  PRIOR FILING DATE:  1998-11-20
;  PRIOR APPLICATION NUMBER:  US 60/066,364
;  PRIOR FILING DATE:  1997-11-21
;  PRIOR APPLICATION NUMBER:  US 60/078,936
;  PRIOR FILING DATE:  1998-03-20
;  PRIOR APPLICATION NUMBER:  PCT/US98/19437
;  PRIOR FILING DATE:  1998-09-17
;  NUMBER OF SEQ ID NOS:  30
; SEQ ID NO 10
;   LENGTH: 300
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;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-907-794A-64

  Query Match             27.9%;  Score 456.5;  DB 4;  Length 312;
  Best Local Similarity   37.1%;  Pred. No. 1.2e-38;
  Matches  104;  Conservative   51;  Mismatches  104;  Indels   21;  Gaps    7;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIG-----AVNLKSSNRTPVVQ--EFESVELSC 53
              || |   ||          |||| |  ::      |    :     ||   |::   |:|
Db          1 MARRSRHRL----------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC 50

Qy         54 IITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALY 113
                |  :|   |:||||:     ::|::   :|||   |||::   :::| |||| |:  |
Db         51 -KTPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107

Qy        114 RCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
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Db        108 RCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

Qy        173 WYRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
              |::: : |  : |   :  |||  :|::|||| |  | | |:|:| | | |  |  ||
Db        168 WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227

Qy        233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYF 272
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Db        228 KRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF 267


RESULT 7
US-09-905-125A-64
; Sequence 64, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION:  Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE:  2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 64
;   LENGTH: 312
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-905-125A-64

  Query Match             27.9%;  Score 456.5;  DB 4;  Length 312;
  Best Local Similarity   37.1%;  Pred. No. 1.2e-38;
  Matches  104;  Conservative   51;  Mismatches  104;  Indels   21;  Gaps    7;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIG-----AVNLKSSNRTPVVQ--EFESVELSC 53
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Db          1 MARRSRHRL----------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC 50

Qy         54 IITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALY 113
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;  EARLIER FILING DATE: 1997-06-06
;  EARLIER APPLICATION NUMBER: 60/068,368
;  EARLIER FILING DATE: 1997-12-19
;  NUMBER OF SEQ ID NOS: 118
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 76
;    LENGTH: 298
;    TYPE: PRT
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: SITE
;    LOCATION: (42)
;    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
;    FEATURE:
;    NAME/KEY: SITE
;    LOCATION: (58)
;    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-152-060-76

  Query Match             29.1%;  Score 476;  DB 4;  Length 298;
  Best Local Similarity   35.8%;  Pred. No. 1.1e-40;
  Matches  114;  Conservative   59;  Mismatches  117;  Indels   28;  Gaps   10;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIG-----AVNLKSSNRTPVVQ--EFESVELSC 53
              || |   ||           |||| |  ::      |    :     ||   ::   |:|
Db          1 MARRSRHRL----------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC 50

Qy         54 IITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALY 113
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Db         51 -KTPKKTVXSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107

Qy        114 RCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
              |||| | ::: : ::|  : | | | |  | | || :  | :  | ||: ||:| | |:
Db        108 RCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

Qy        173 WYRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
              |::: : |  : |   :  |||  :|::|||| |  | | |:|:| | | |  |  ||
Db        168 WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227

Qy        233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVN 292
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Qy        293 YIRTDEEGDFRHKSSFVI 310
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Db        281 KATTMSENDFKHTKSFII 298


RESULT 5
US-09-254-465A-9
; Sequence 9, Application US/09254465A
; Patent No. 6410708
; GENERAL INFORMATION:
;  APPLICANT:  Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi J.
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION:  COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
;  TITLE OF INVENTION:  OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
;  FILE REFERENCE:  P1216R1(US)
;  CURRENT APPLICATION NUMBER: US/09/254,465A
;  CURRENT FILING DATE:  1999-03-05
;  PRIOR APPLICATION NUMBER:  PCT/US98/24855
;  PRIOR FILING DATE:  1998-11-20
;  PRIOR APPLICATION NUMBER:  US 60/066,364
;  PRIOR FILING DATE:  1997-11-21
;  PRIOR APPLICATION NUMBER:  US 60/078,936
;  PRIOR FILING DATE:  1998-03-20
;  PRIOR APPLICATION NUMBER:  PCT/US98/19437
;  PRIOR FILING DATE:  1998-09-17
;  NUMBER OF SEQ ID NOS:  30
; SEQ ID NO 9
;    LENGTH: 312
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-254-465A-9

  Query Match             27.9%;  Score 456.5;  DB 4;  Length 312;
  Best Local Similarity   37.1%;  Pred. No. 1.2e-38;
  Matches  104;  Conservative   51;  Mismatches  104;  Indels   21;  Gaps    7;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIG-----AVNLKSSNRTPVVQ--EFESVELSC 53
              || |   ||           |||| |  ::      |    :     ||   ::   |:|
Db          1 MARRSRHRL----------LLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILAC 50

Qy         54 IITDSQTSDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALY 113
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Db         51 -KTPKKTVSSRLEWKKL-GRSVSFVYYQQTLQGDFKNRAEMI-DFNIRIKNVTRSDAGKY 107

Qy        114 RCEVVARNDR-KEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYS 172
              |||| | ::: : ::|  : | | | |  | | || :  | :  | ||: ||:| | |:
Db        108 RCEVSAPSEQGQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYT 167

Qy        173 WYRNDVPLPTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEE 232
              |::: : |  : |   :  |||  :|::|||| |  | | |:|:| | | |  |  ||
Db        168 WFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVGYRRCPG 227

Qy        233 QEMEVYDLNIGGIIGGVLVVLAVLALITLGICCAYRRGYF 272
              : |:| |||| |||  |:||  |:::  ||:| | |:|||
Db        228 KRMQVDDLNISGIIAAVVVVALVISVCGLGVCYAQRKGYF 267


RESULT 6
US-09-907-794A-64
; Sequence 64, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/907,794A
;  CURRENT FILING DATE:  2001-07-17
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
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Qy        301 DFRHKSSFVI 310
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Db        301 DFRHKSSFVI 310


RESULT 3
US-09-902-775A-423
; Sequence 423, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/902,775A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-902-775A-423

  Query Match             99.6%;  Score 1629;  DB 4;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 2.8e-159;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
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Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
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Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
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Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
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Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
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Db        301 DFRHKSSFVI 310


RESULT 4
US-09-152-060-76
; Sequence 76, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: 28 Human Secreted Proteins
;  FILE REFERENCE: PZ003P1.US
;  CURRENT APPLICATION NUMBER: US/09/152,060
;  CURRENT FILING DATE: 1998-09-11
;  EARLIER APPLICATION NUMBER: PCT/US98/04858
;  EARLIER FILING DATE: 1998-03-12
;  EARLIER APPLICATION NUMBER: 60/040,762
;  EARLIER FILING DATE: 1997-03-14
;  EARLIER APPLICATION NUMBER: 60/040,710
;  EARLIER FILING DATE: 1997-03-14
;  EARLIER APPLICATION NUMBER: 60/050,934
;  EARLIER FILING DATE: 1997-05-30
;  EARLIER APPLICATION NUMBER: 60/048,100
;  EARLIER FILING DATE: 1997-05-30
;  EARLIER APPLICATION NUMBER: 60/048,357
;  EARLIER FILING DATE: 1997-05-30
;  EARLIER APPLICATION NUMBER: 60/048,189
;  EARLIER FILING DATE: 1997-05-30
;  EARLIER APPLICATION NUMBER: 60/057,765
;  EARLIER FILING DATE: 1997-09-05
;  EARLIER APPLICATION NUMBER: 60/048,970
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;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-907-794A-423

  Query Match             99.6%;  Score 1629;  DB 4;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 2.8e-159;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
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Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
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Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
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Qy        301 DFRHKSSFVI 310
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Db        301 DFRHKSSFVI 310


RESULT 2
US-09-905-125A-423
; Sequence 423, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/905,125A
;  CURRENT FILING DATE:  2001-07-12
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: PCT/US99/20594
;  PRIOR FILING DATE: 1999-09-08
;  PRIOR APPLICATION NUMBER: PCT/US99/20944
;  PRIOR FILING DATE: 1999-09-13
;  PRIOR APPLICATION NUMBER: PCT/US99/21090
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/21547
;  PRIOR FILING DATE: 1999-09-15
;  PRIOR APPLICATION NUMBER: PCT/US99/23089
;  PRIOR FILING DATE: 1999-10-05
;  PRIOR APPLICATION NUMBER: PCT/US99/28214
;  PRIOR FILING DATE: 1999-11-29
;  PRIOR APPLICATION NUMBER: PCT/US99/28313
;  PRIOR FILING DATE: 1999-11-30
;  PRIOR APPLICATION NUMBER: PCT/US99/28564
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/28565
;  PRIOR FILING DATE: 1999-12-02
;  PRIOR APPLICATION NUMBER: PCT/US99/30095
;  PRIOR FILING DATE: 1999-12-16
;  PRIOR APPLICATION NUMBER: PCT/US99/30911
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-905-125A-423

  Query Match             99.6%;  Score 1629;  DB 4;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 2.8e-159;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
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Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:14:48 ; Search time 22 Seconds
(without alignments)
727.457 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 1635
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1629	99.6	310	4	US-09-907-794A-423	Sequence 423, App
2	1629	99.6	310	4	US-09-905-125A-423	Sequence 423, App
3	1629	99.6	310	4	US-09-902-775A-423	Sequence 423, App
4	476	29.1	298	4	US-09-152-060-76	Sequence 76, Appl
5	456.5	27.9	312	4	US-09-254-465A-9	Sequence 9, Appli
6	456.5	27.9	312	4	US-09-907-794A-64	Sequence 64, Appl
7	456.5	27.9	312	4	US-09-905-125A-64	Sequence 64, Appl
8	456.5	27.9	312	4	US-09-902-775A-64	Sequence 64, Appl
9	449.5	27.5	300	4	US-09-254-465A-10	Sequence 10, Appl
10	419	25.6	299	3	US-09-188-930-331	Sequence 331, App
11	419	25.6	299	4	US-09-462-270-2	Sequence 2, Appli
12	419	25.6	299	4	US-09-254-465A-1	Sequence 1, Appli
13	419	25.6	299	4	US-09-312-283C-189	Sequence 189, App
14	419	25.6	299	4	US-09-312-283C-331	Sequence 331, App
15	419	25.6	299	4	US-09-907-794A-119	Sequence 119, App
16	419	25.6	299	4	US-09-905-125A-119	Sequence 119, App
17	419	25.6	299	4	US-09-902-775A-119	Sequence 119, App
18	407	24.9	299	3	US-09-188-930-189	Sequence 189, App
19	387.5	23.7	260	4	US-09-254-465A-23	Sequence 23, Appl
20	387.5	23.7	263	4	US-09-254-465A-25	Sequence 25, Appl
21	283	17.3	205	4	US-09-462-270-4	Sequence 4, Appli
22	231.5	14.2	319	1	US-08-597-495B-22	Sequence 22, Appl
23	231.5	14.2	319	3	US-09-068-051A-22	Sequence 22, Appl
24	231.5	14.2	319	4	US-09-336-536-67	Sequence 67, Appl
25	231.5	14.2	319	4	US-09-254-465A-6	Sequence 6, Appli
26	220.5	13.5	270	4	US-09-254-465A-24	Sequence 24, Appl
27	220.5	13.5	273	4	US-09-254-465A-26	Sequence 26, Appl
28	215.5	13.2	318	3	US-09-068-051A-32	Sequence 32, Appl
29	198.5	12.1	387	4	US-09-175-928-2	Sequence 2, Appli
30	175.5	10.7	370	4	US-09-336-536-28	Sequence 28, Appl
31	171.5	10.5	390	2	US-08-979-424-1	Sequence 1, Appli
32	171.5	10.5	390	4	US-09-907-794A-39	Sequence 39, Appl
33	171.5	10.5	390	4	US-09-905-125A-39	Sequence 39, Appl
34	171.5	10.5	390	4	US-09-902-775A-39	Sequence 39, Appl
35	171.5	10.5	394	4	US-09-336-536-39	Sequence 39, Appl
36	168.5	10.3	341	4	US-09-336-536-29	Sequence 29, Appl
37	168.5	10.3	398	4	US-09-778-510-6	Sequence 6, Appli
38	168.5	10.3	398	4	US-09-907-794A-84	Sequence 84, Appl
39	168.5	10.3	398	4	US-09-905-125A-84	Sequence 84, Appl
40	168.5	10.3	398	4	US-09-902-775A-84	Sequence 84, Appl
41	167	10.2	365	4	US-09-336-536-40	Sequence 40, Appl
42	164.5	10.1	246	4	US-09-336-536-31	Sequence 31, Appl
43	164.5	10.1	365	3	US-08-928-383B-2	Sequence 2, Appli
44	161.5	9.9	365	2	US-08-979-424-3	Sequence 3, Appli
45	161.5	9.9	365	3	US-09-272-496-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-907-794A-423
; Sequence 423, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

ALIGNMENTS

RESULT 1
US-09-907-794A-423
; Sequence 423, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-794A-423

Query Match 67.4%; Score 209; DB 4; Length 310;
Best Local Similarity 99.7%; Pred. No. 1e-185;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; Sequence 423, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414

GenCore version 5.1.6

OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 389414

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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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88	6	1.9	72	4	US-09-621-976-5214	Sequence 5214, Ap
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91	6	1.9	76	1	US-08-519-777-22	Sequence 22, Appl
92	6	1.9	76	1	US-08-742-035-22	Sequence 22, Appl
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97	6	1.9	76	3	US-08-981-739-22	Sequence 22, Appl
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ALIGNMENTS

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RESULT 1
US-09-909-320-423
; Sequence 423, Application US/09909320
; Patent No. US20020132240A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, A.
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William, I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: 10466-14
;  CURRENT APPLICATION NUMBER: US/09/909,320
;  CURRENT FILING DATE:  2002-01-04
;  PRIOR APPLICATION NUMBER: PCT/US00/04414
;  PRIOR FILING DATE: 2000-02-22
;  PRIOR APPLICATION NUMBER: US 60/143,048
;  PRIOR FILING DATE: 1999-07-07
;  PRIOR APPLICATION NUMBER: US 60/145,698
;  PRIOR FILING DATE: 1999-07-26
;  PRIOR APPLICATION NUMBER: US 60/146,222
;  PRIOR FILING DATE: 1999-07-28
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;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US99/30999
;  PRIOR FILING DATE: 1999-12-20
;  PRIOR APPLICATION NUMBER: PCT/US00/00219
;  PRIOR FILING DATE: 2000-01-05
;  NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 423
;   LENGTH: 310
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-09-909-320-423

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Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
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RESULT 2
US-09-909-088B-423
; Sequence 423, Application US/09909088B
; Patent No. US20020146709A1
; GENERAL INFORMATION:
;  APPLICANT: Genentech, Inc.
;  APPLICANT:  Ashkenazi, Avi
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan L.
;  APPLICANT:  Ferrara, Napoleone
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
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;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
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;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, Christopher J.
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth, J.
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Mather, Jennie P.
;  APPLICANT:  Pan, James
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:24:55 ; Search time 46 Seconds
(without alignments)
1771.973 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1073127 seqs, 262937947 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	209	67.4	310	9	US-09-909-320-423	Sequence 423, App
2	209	67.4	310	9	US-09-909-088B-423	Sequence 423, App
3	209	67.4	310	9	US-09-905-291A-423	Sequence 423, App
4	209	67.4	310	9	US-09-902-853-423	Sequence 423, App
5	209	67.4	310	9	US-09-907-824-423	Sequence 423, App
6	209	67.4	310	9	US-09-907-841-423	Sequence 423, App
7	209	67.4	310	10	US-09-904-011-423	Sequence 423, App
8	209	67.4	310	10	US-09-906-742-423	Sequence 423, App
9	209	67.4	310	10	US-09-906-838-423	Sequence 423, App
10	209	67.4	310	10	US-09-907-613-423	Sequence 423, App
11	209	67.4	310	10	US-09-907-942-423	Sequence 423, App
12	209	67.4	310	10	US-09-904-859-423	Sequence 423, App
13	209	67.4	310	10	US-09-909-204-423	Sequence 423, App
14	209	67.4	310	10	US-09-904-820-423	Sequence 423, App
15	209	67.4	310	10	US-09-904-786-423	Sequence 423, App
16	209	67.4	310	10	US-09-906-646-423	Sequence 423, App
17	209	67.4	310	10	US-09-906-700-423	Sequence 423, App
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19	209	67.4	310	10	US-09-902-903-423	Sequence 423, App
20	209	67.4	310	10	US-09-903-749A-423	Sequence 423, App
21	209	67.4	310	10	US-09-904-119-423	Sequence 423, App
22	209	67.4	310	10	US-09-904-956-423	Sequence 423, App
23	209	67.4	310	10	US-09-902-736-423	Sequence 423, App
24	209	67.4	310	10	US-09-907-794-423	Sequence 423, App
25	209	67.4	310	10	US-09-903-943-423	Sequence 423, App
26	209	67.4	310	10	US-09-904-462-423	Sequence 423, App
27	209	67.4	310	10	US-09-907-925-423	Sequence 423, App
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33	209	67.4	310	10	US-09-905-381-423	Sequence 423, App
34	209	67.4	310	10	US-09-905-088-423	Sequence 423, App
35	209	67.4	310	10	US-09-907-575-423	Sequence 423, App
36	209	67.4	310	10	US-09-905-075-423	Sequence 423, App
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42	209	67.4	310	10	US-09-903-925-423	Sequence 423, App
43	209	67.4	310	10	US-09-906-760A-423	Sequence 423, App
44	209	67.4	310	10	US-09-903-823-423	Sequence 423, App
45	209	67.4	310	10	US-09-907-652-423	Sequence 423, App
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59	209	67.4	310	10	US-09-866-034-20	Sequence 20, Appl
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62	209	67.4	310	10	US-09-906-618-423	Sequence 423, App
63	209	67.4	310	10	US-09-907-728-423	Sequence 423, App
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67	209	67.4	310	11	US-09-908-576-423	Sequence 423, App
68	209	67.4	310	11	US-09-833-245-2045	Sequence 2045, Ap
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70	209	67.4	310	11	US-09-833-245-2047	Sequence 2047, Ap
71	209	67.4	310	12	US-10-147-493-538	Sequence 538, App
72	209	67.4	310	12	US-10-145-127-538	Sequence 538, App
73	209	67.4	310	12	US-10-160-503-538	Sequence 538, App
74	209	67.4	310	12	US-10-143-118-538	Sequence 538, App
75	209	67.4	310	12	US-10-144-993-538	Sequence 538, App
76	209	67.4	310	12	US-10-158-787-538	Sequence 538, App
77	209	67.4	310	12	US-10-081-056-262	Sequence 262, App
78	209	67.4	310	12	US-10-140-024-538	Sequence 538, App
79	209	67.4	310	13	US-10-033-246-20	Sequence 20, Appl
80	209	67.4	310	13	US-10-033-301-20	Sequence 20, Appl
81	209	67.4	310	13	US-10-033-326-20	Sequence 20, Appl
82	209	67.4	310	13	US-10-033-245-20	Sequence 20, Appl
83	209	67.4	310	13	US-10-033-223-20	Sequence 20, Appl
84	209	67.4	310	13	US-10-033-167-20	Sequence 20, Appl
85	209	67.4	310	13	US-10-033-244-20	Sequence 20, Appl
86	209	67.4	310	14	US-10-028-072-538	Sequence 538, App
87	209	67.4	310	14	US-10-121-049-538	Sequence 538, App
88	209	67.4	310	14	US-10-123-904-538	Sequence 538, App

99	209	67.4	310	7	ADB18435	Adb18435 Human PRO
100	209	67.4	310	7	ADA87118	Ada87118 Novel hum

ALIGNMENTS

```
RESULT 1
AAY96294
ID   AAY96294 standard; protein; 310 AA.
XX
AC   AAY96294;
XX
DT   16-AUG-2000  (first entry)
XX
DE   Human IGFAM-6 immunoglobulin.
XX
KW   Human; immunoglobulin; IGFAM-6; IGFAM; immune disorder; cancer;
KW   infection; inflammation; haematopoiesis; AIDS; allergy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .30
FT                   /label= signal_peptide
FT   Protein         31. .310
FT                   /label= IGFAM-6
FT   Domain          46. .117
FT                   /label= Ig_domain
FT   Domain          153. .221
FT                   /label= Ig_domain
FT   Domain          238. .260
FT                   /label= transmembrane_domain
XX
PN   WO200029583-A2.
XX
PD   25-MAY-2000.
XX
PF   19-NOV-1999;   99WO-US027566.
XX
PR   19-NOV-1998;   98US-00195853.
PR   22-DEC-1998;   98US-0113635P.
PR   07-APR-1999;   99US-0128194P.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Yue H,  Tang YT,  Corley NC,  Guegler KJ,  Gorgone GA,  Baughn MR;
PI   Lu DAM,  Lal P,  Hillman JL,  Yang J;
XX
DR   WPI; 2000-387796/33.
DR   N-PSDB; AAA27386.
XX
PT   Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT   protein is useful for preventing and treating disorders associated with
PT   altered levels of the protein such as cancer, immune system disorders.
XX
PS   Claim 1; Page 82-83; 105pp; English.
XX
CC   The present sequence is the human immunoglobulin superfamily protein
CC   IGFAM-6. Its gene was isolated from a cDNA library of leg tissue. It is
CC   expressed in reproductive, nervous and cardiovascular tissue, where
CC   cancer and inflammation are common. The gene, protein, its antibodies,
CC   agonists and antagonists are suitable for diagnosing and treating many
CC   diseases, including cancer, immune system disorders (such as
CC   inflammation, AIDS, allergies, anaemia, arteriosclerosis, asthma,
CC   atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus,
CC   emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis,
CC   rheumatoid arthritis, scleroderma, systemic lupus erythematosus and
CC   ulcerative colitis), complications of cancer, haemodialysis and
CC   extracorporeal circulation, trauma and haematopoietic cancer (such as
CC   leukaemia) and infections caused by bacteria, viruses, fungi or parasites
XX
SQ   Sequence 310 AA;
```

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  Query Match             100.0%;  Score 310;  DB 3;  Length 310;
  Best Local Similarity   100.0%;  Pred. No. 4.3e-296;
  Matches  310;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310
```

```
RESULT 2
AAY96735
ID   AAY96735 standard; protein; 310 AA.
XX
AC   AAY96735;
XX
DT   26-SEP-2000  (first entry)
XX
DE   PRO1868, an A33 antigen homologue.
XX
KW   PRO1868; A33 antigen; secreted protein; transmembrane protein;
KW   anti-inflammatory; cytostatic; recombinant production; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .30
FT                   /label= Signal_peptide
FT   Modified-site   26. .31
FT                   /note= "N-myristoylation site"
FT   Modified-site   69. .77
FT                   /note= "Tyrosine kinase phosphorylation site"
FT   Modified-site   104. .107
FT                   /note= "N-glycosylation site"
FT   Modified-site   106. .109
FT                   /note= "Casein kinase II phosphorylation site"
FT   Modified-site   107. .110
FT                   /note= "cAMP- and cGMP-dependent protein kinase
FT                   phosphorylation site"
FT   Modified-site   192. .195
FT                   /note= "N-glycosylation site"
FT   Modified-site   215. .220
FT                   /note= "N-myristoylation site"
FT   Modified-site   226. .231
FT                   /note= "N-myristoylation site"
FT   Domain          243. .263
FT                   /label= Transmembrane_domain
FT   Modified-site   243. .248
FT                   /note= "N-myristoylation site"
FT   Modified-site   244. .249
FT                   /note= "N-myristoylation site"
FT   Modified-site   262. .267
FT                   /note= "N-myristoylation site"
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:16:49 ; Search time 60 Seconds
(without alignments)
1459.829 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	310	100.0	310	3	AAY96294	Aay96294 Human IGF
2	209	67.4	310	3	AAY96735	Aay96735 PRO1868,
3	209	67.4	310	3	AAB33457	Aab33457 Human PRO
4	209	67.4	310	3	AAB27276	Aab27276 Human con
5	209	67.4	310	4	AAB80272	Aab80272 Human PRO
6	209	67.4	310	4	AAM93905	Aam93905 Human pol
7	209	67.4	310	4	AAM93323	Aam93323 Human pol
8	209	67.4	310	4	AAU12440	Aau12440 Human PRO
9	209	67.4	310	4	AAB80383	Aab80383 Secreted
10	209	67.4	310	4	AAB80408	Aab80408 Secreted
11	209	67.4	310	4	AAB80409	Aab80409 Secreted
12	209	67.4	310	5	ABG92709	Abg92709 Human sec
13	209	67.4	310	5	ABG91361	Abg91361 Novel hum
14	209	67.4	310	5	ABB84947	Abb84947 Human PRO
15	209	67.4	310	5	ABG65297	Abg65297 Human alb
16	209	67.4	310	5	ABG65296	Abg65296 Human alb
17	209	67.4	310	5	ABG65298	Abg65298 Human alb
18	209	67.4	310	5	ABG31401	Abg31401 Human PRO
19	209	67.4	310	5	ABB95553	Abb95553 Human ang
20	209	67.4	310	6	ABU71650	Abu71650 Human PRO
21	209	67.4	310	6	ABU72377	Abu72377 Novel hum
22	209	67.4	310	6	ABU80867	Abu80867 Human sec
23	209	67.4	310	6	ABO17884	Abo17884 Novel hum
24	209	67.4	310	6	ABU71505	Abu71505 Human PRO
25	209	67.4	310	6	ADA57610	Ada57610 Human sec
26	209	67.4	310	6	ADA57611	Ada57611 Human sec
27	209	67.4	310	6	ADA57309	Ada57309 Human sec
28	209	67.4	310	6	ABP71277	Abp71277 Human jun
29	209	67.4	310	6	ABU81138	Abu81138 Human PRO
30	209	67.4	310	6	ABU71951	Abu71951 Human sec
31	209	67.4	310	6	ABO01834	Abo01834 Novel hum
32	209	67.4	310	6	ABU66838	Abu66838 Human PRO
33	209	67.4	310	6	ABU54407	Abu54407 Human sec
34	209	67.4	310	6	ABO47422	Abo47422 Human sec
35	209	67.4	310	6	ABG73314	Abg73314 Human PRO
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39	209	67.4	310	6	ABU67405	Abu67405 Human sec
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43	209	67.4	310	6	ABU81236	Abu81236 Human PRO
44	209	67.4	310	6	ABU69682	Abu69682 Novel hum
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46	209	67.4	310	6	ADA46057	Ada46057 Novel hum
47	209	67.4	310	6	ADA76488	Ada76488 Human PRO
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49	209	67.4	310	6	ADA19138	Ada19138 Human PRO
50	209	67.4	310	6	ADA61761	Ada61761 Homo sapi
51	209	67.4	310	6	ADB19546	Adb19546 Novel hum
52	209	67.4	310	6	ADB28087	Adb28087 Human PRO
53	209	67.4	310	6	ADA86566	Ada86566 Novel hum
54	209	67.4	310	6	ADB16130	Adb16130 Human PRO
55	209	67.4	310	6	ADA47916	Ada47916 Human PRO
56	209	67.4	310	6	ADA18484	Ada18484 Human sec
57	209	67.4	310	6	ABO32816	Abo32816 Human sec
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59	209	67.4	310	6	ADB30718	Adb30718 Human PRO
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61	209	67.4	310	6	ADA97226	Ada97226 Human PRO
62	209	67.4	310	6	ADA79530	Ada79530 Human PRO
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64	209	67.4	310	6	ADB16871	Adb16871 Human PRO
65	209	67.4	310	6	ABO34876	Abo34876 Human PRO
66	209	67.4	310	6	ADA16459	Ada16459 Human sec
67	209	67.4	310	6	ADA91963	Ada91963 Novel hum
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69	209	67.4	310	6	ADB18987	Adb18987 Novel hum
70	209	67.4	310	6	ADA94202	Ada94202 Human PRO
71	209	67.4	310	6	ADB20098	Adb20098 Novel hum
72	209	67.4	310	6	ADB13410	Adb13410 Human PRO
73	209	67.4	310	6	ABO43417	Abo43417 Novel hum
74	209	67.4	310	6	ADA74664	Ada74664 Human PRO
75	209	67.4	310	6	ADA42604	Ada42604 Human sec
76	209	67.4	310	6	ADB24897	Adb24897 Human PRO
77	209	67.4	310	6	ADA82421	Ada82421 Human PRO
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82	209	67.4	310	6	ADB30166	Adb30166 Human PRO
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84	209	67.4	310	6	ADA75936	Ada75936 Human PRO
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86	209	67.4	310	6	ADB25457	Adb25457 Human PRO
87	209	67.4	310	6	ADA93633	Ada93633 Human PRO
88	209	67.4	310	6	ADB26983	Adb26983 Human PRO
89	209	67.4	310	6	ADB31270	Adb31270 Human PRO
90	209	67.4	310	6	ABU62957	Abu62957 Human PRO
91	209	67.4	310	6	ADA61198	Ada61198 Homo sapi
92	209	67.4	310	6	ADB24345	Adb24345 Human PRO
93	209	67.4	310	6	ADA96674	Ada96674 Human PRO
94	209	67.4	310	6	ADA81246	Ada81246 Human PRO
95	209	67.4	310	6	ADA96122	Ada96122 Human PRO
96	209	67.4	310	6	ADB26431	Adb26431 Human PRO
97	209	67.4	310	6	ADB21916	Adb21916 Novel hum
98	209	67.4	310	7	ADA77695	Ada77695 Human PRO

90	7	2.3	210	16	Q8DSW6	Q8dsw6 streptococc
91	7	2.3	211	16	Q9CDV2	Q9cdv2 lactococcus
92	7	2.3	214	2	O32618	O32618 helicobacte
93	7	2.3	214	6	O62722	O62722 oryctolagus
94	7	2.3	215	16	Q837X2	Q837x2 enterococcu
95	7	2.3	217	12	Q9YMN1	Q9ymn1 lymantria d
96	7	2.3	219	16	Q8KDL2	Q8kdl2 chlorobium
97	7	2.3	221	11	Q8C8M1	Q8c8m1 mus musculu
98	7	2.3	224	11	Q9R1M6	Q9r1m6 mus musculu
99	7	2.3	227	12	Q91BE2	Q91be2 spodoptera
100	7	2.3	229	16	Q8FR05	Q8fr05 corynebacte

ALIGNMENTS

```
RESULT 1
Q9BX67
ID   Q9BX67      PRELIMINARY;      PRT;   310 AA.
AC   Q9BX67;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junctional adhesion molecule 3 precursor (Junctional adhesion
DE   molecule-2) (Junctional adhesional molecule-3) (Hypothetical protein
DE   FLJ90288) (Hypothetical protein FLJ90828).
GN   JAM-2 OR JAM3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Cunningham S.A., Arrate M.P., Tran T.M.;
RT   "Cloning of Human Junctional Adhesion Molecule 3.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Aurrand-Lions M.A., Johnson-leger C., Wong C., DuPasquier L.;
RT   "Heterogeneity of endothelial junctions is reflected by differential
RT   expression and specific subcellular localization of the three JAM
RT   family members.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Aurrand-Lions M.A., Johnson-leger C., Lamagna C., Ozaki H., Kita T.;
RT   "Junctional adhesion molecules (JAMs) and interendothelial
RT   junctions.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Sachs U.J.H., Eva O., Berghoefer H., Santoso S.;
RT   "Characterization of Junctional Adhesional Molecule-3 on Human
RT   Platelets: A New Member of Immunoglobulin Superfamily.";
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A.
RA   Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA   Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA   Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA   Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA   Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF356518; AAK27221.1; -.
DR   EMBL; AJ344431; CAC69845.1; -.
DR   EMBL; AF448478; AAM20925.1; -.
DR   EMBL; AK074769; BAC11195.1; -.
DR   EMBL; AK075309; BAC11538.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein; Signal.
FT   SIGNAL       1     30       POTENTIAL.
SQ   SEQUENCE   310 AA;  35020 MW;  CE39ADF33EA1DAB9 CRC64;

  Query Match             67.4%;  Score 209;  DB 4;  Length 310;
  Best Local Similarity   99.7%;  Pred. No. 3.2e-214;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60

Qy         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SDPRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVAR 120

Qy        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 NDRKEIDEIVIELTVQVKPVTPVCRVPKAVPVGKMATLHCQESEGHPRPHYSWYRNDVPL 180

Qy        181 PTDSRANPRFRNSSSHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        181 PTDSRANPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDL 240

Qy        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NIGGIIGGVLVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEG 300

Qy        301 DFRHKSSFVI 310
              ||||||||||
Db        301 DFRHKSSFVI 310


RESULT 2
Q8WWL8
ID   Q8WWL8      PRELIMINARY;      PRT;   355 AA.
AC   Q8WWL8;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Junction adhesion molecule 3.
GN   JAM3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hearn T.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Phillips H.M.;
RT   "Narrowing the critical region within 11q24-qter for hypoplastic left
RT   heart and identification of a candidate gene, JAM3, expressed during
RT   cardiogenesis.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ416101; CAC94776.1; -.
DR   Genew; HGNC:15532; JAM3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain.
FT   CHAIN        76    355       JUNCTION ADHESION MOLECULE 3.
SQ   SEQUENCE   355 AA;  39602 MW;  8B1577DEA7B1D4F8 CRC64;

  Query Match             67.4%;  Score 209;  DB 4;  Length 355;
  Best Local Similarity   99.7%;  Pred. No. 3.7e-214;
  Matches  309;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQT 60
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:20:39 ; Search time 46 Seconds
(without alignments)
2126.318 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	209	67.4	310	4	Q9BX67	Q9bx67 homo sapien
2	209	67.4	355	4	Q8WWL8	Q8wwl8 homo sapien
3	134	43.2	309	4	Q96FL1	Q96fl1 homo sapien
4	32	10.3	310	11	Q9D8B7	Q9d8b7 mus musculu
5	28	9.0	310	11	Q9D1M9	Q9d1m9 mus musculu
6	28	9.0	310	11	Q9EPK4	Q9epk4 mus musculu
7	13	4.2	64	11	Q8BT59	Q8bt59 mus musculu
8	8	2.6	39	7	Q9TNT2	Q9tnt2 homo sapien
9	8	2.6	67	7	Q8HWG1	Q8hwg1 homo sapien
10	8	2.6	76	5	Q867W1	Q867w1 procambarus
11	8	2.6	131	5	Q8I8S1	Q8i8s1 anopheles g
12	8	2.6	154	11	Q8C4V2	Q8c4v2 mus musculu
13	8	2.6	231	16	Q89E35	Q89e35 bradyrhizob
14	8	2.6	231	17	Q8TQT5	Q8tqt5 methanosarc
15	8	2.6	232	17	Q8ZSR8	Q8zsr8 pyrobaculum
16	8	2.6	233	10	Q9LR49	Q9lr49 arabidopsis
17	8	2.6	246	5	Q966C0	Q966c0 caenorhabdi
18	8	2.6	294	16	Q98EQ9	Q98eq9 rhizobium l
19	8	2.6	309	5	Q9N4Y9	Q9n4y9 caenorhabdi
20	8	2.6	322	2	Q9RPI7	Q9rpi7 desulfitoba
21	8	2.6	336	10	Q9C7E9	Q9c7e9 arabidopsis
22	8	2.6	338	7	Q9MXL5	Q9mxl5 pan troglod
23	8	2.6	348	7	Q9MWJ9	Q9mwj9 gorilla gor
24	8	2.6	348	16	Q9PR46	Q9pr46 ureaplasma
25	8	2.6	363	7	Q95HC2	Q95hc2 homo sapien
26	8	2.6	365	7	Q9XRX8	Q9xrx8 pongo pygma
27	8	2.6	365	7	Q9XRX7	Q9xrx7 pongo pygma
28	8	2.6	365	7	Q9MXG4	Q9mxg4 pan troglod
29	8	2.6	366	6	O46684	O46684 pan troglod
30	8	2.6	366	7	Q8MHH0	Q8mhh0 pongo pygma
31	8	2.6	366	7	Q8MHH1	Q8mhh1 pongo pygma
32	8	2.6	366	7	Q8MHG8	Q8mhg8 pongo pygma
33	8	2.6	366	7	Q8MHG9	Q8mhg9 pongo pygma
34	8	2.6	366	7	O19617	O19617 homo sapien
35	8	2.6	366	7	Q860B0	Q860b0 homo sapien
36	8	2.6	366	7	Q85ZX8	Q85zx8 homo sapien
37	8	2.6	366	7	Q9TPL2	Q9tpl2 pan troglod
38	8	2.6	366	7	Q9MXD2	Q9mxd2 pan troglod
39	8	2.6	366	7	Q7YQB2	Q7yqb2 homo sapien
40	8	2.6	449	16	Q8CWZ7	Q8cwz7 streptococc
41	8	2.6	452	16	Q8G5D2	Q8g5d2 bifidobacte
42	8	2.6	492	16	Q8Z1U9	Q8z1u9 salmonella
43	8	2.6	659	16	Q8EK37	Q8ek37 shewanella
44	8	2.6	784	16	Q9CIF4	Q9cif4 lactococcus
45	8	2.6	1290	13	Q9W6E1	Q9w6e1 gallus gall
46	7	2.3	67	4	Q8NI85	Q8ni85 homo sapien
47	7	2.3	82	16	Q837K2	Q837k2 enterococcu
48	7	2.3	85	12	Q99GX8	Q99gx8 helicoverpa
49	7	2.3	86	16	Q8ERD1	Q8erd1 oceanobacil
50	7	2.3	92	10	Q8LFP4	Q8lfp4 arabidopsis
51	7	2.3	92	10	Q8GXY9	Q8gxy9 arabidopsis
52	7	2.3	100	10	Q84QM7	Q84qm7 oryza sativ
53	7	2.3	104	9	Q8W6S9	Q8w6s9 bacteriopha
54	7	2.3	112	16	Q8CSN1	Q8csn1 staphylococ
55	7	2.3	113	16	Q928J9	Q928j9 listeria in
56	7	2.3	116	17	Q8U327	Q8u327 pyrococcus
57	7	2.3	135	2	Q8RJT0	Q8rjt0 streptococc
58	7	2.3	144	10	Q8LN01	Q8ln01 oryza sativ
59	7	2.3	144	16	Q81KV1	Q81kv1 bacillus an
60	7	2.3	146	17	Q973F7	Q973f7 sulfolobus
61	7	2.3	148	16	Q82IL9	Q82il9 streptomyce
62	7	2.3	149	6	Q7YS63	Q7ys63 sus scrofa
63	7	2.3	155	16	Q88BJ0	Q88bj0 pseudomonas
64	7	2.3	158	2	Q9EWB3	Q9ewb3 streptomyce
65	7	2.3	158	16	Q8XSK1	Q8xsk1 ralstonia s
66	7	2.3	163	9	Q7Y514	Q7y514 bacteriopha
67	7	2.3	166	2	Q8GD28	Q8gd28 bordetella
68	7	2.3	168	16	Q897J4	Q897j4 clostridium
69	7	2.3	171	16	O06422	O06422 mycobacteri
70	7	2.3	171	16	Q7U1S3	Q7u1s3 mycobacteri
71	7	2.3	172	10	Q9SZQ8	Q9szq8 arabidopsis
72	7	2.3	173	5	Q22966	Q22966 caenorhabdi
73	7	2.3	173	10	O64567	O64567 arabidopsis
74	7	2.3	173	17	Q97ZK3	Q97zk3 sulfolobus
75	7	2.3	177	16	Q931Y0	Q931y0 staphylococ
76	7	2.3	177	16	Q8X7L2	Q8x7l2 escherichia
77	7	2.3	179	16	Q9RKC2	Q9rkc2 streptomyce
78	7	2.3	189	17	Q8TMY8	Q8tmy8 methanosarc
79	7	2.3	191	10	Q9XHM2	Q9xhm2 medicago tr
80	7	2.3	194	16	Q8EZ34	Q8ez34 leptospira
81	7	2.3	200	10	Q8VYT4	Q8vyt4 arabidopsis
82	7	2.3	201	16	Q83N81	Q83n81 tropheryma
83	7	2.3	201	16	Q83FI6	Q83fi6 tropheryma
84	7	2.3	202	6	Q9TUF4	Q9tuf4 propithecus
85	7	2.3	202	6	Q9TUF5	Q9tuf5 cercopithec
86	7	2.3	204	2	Q8KUI4	Q8kui4 actinosynne
87	7	2.3	208	10	O80501	O80501 arabidopsis
88	7	2.3	208	10	Q40525	Q40525 nicotiana t
89	7	2.3	208	10	Q8H4Q9	Q8h4q9 oryza sativ

```
TX3A_PHONI
ID   TX3A_PHONI     STANDARD;      PRT;    80 AA.
AC   P81793;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Neurotoxin Pn3A precursor.
OS   Phoneutria nigriventer (Brazilian armed spider).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC   Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
OX   NCBI_TaxID=6918;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Venom gland;
RX   MEDLINE=99053416; PubMed=9839681;
RA   Kalapothakis E., Penaforte C.L., Leao R.M., Cruz J.S., Prado V.F.,
RA   Cordeiro M.N., Diniz C.R., Romano-Silva M.A., Prado M.A.M.,
RA   Gomez M.V., Beirao P.S.L.;
RT   "Cloning, cDNA sequence analysis and patch clamp studies of a toxin
RT   from the venom of the armed spider (Phoneutria nigriventer).";
RL   Toxicon 36:1971-1980(1998).
CC   -!- FUNCTION: Antagonist of L-type calcium channels (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC   -!- SIMILARITY: Belongs to the spider toxin Tx3 family.
DR   InterPro; IPR004169; spidertoxin.
DR   Pfam; PF02819; spidertoxin; 1.
KW   Calcium channel inhibitor; Toxin; Neurotoxin; Ionic channel inhibitor;
KW   Signal.
FT   SIGNAL        1     21       POTENTIAL.
FT   PROPEP       22     37       BY SIMILARITY.
FT   CHAIN        38     71       NEUROTOXIN PN3A.
FT   PROPEP       72     80       BY SIMILARITY.
SQ   SEQUENCE   80 AA;  8937 MW;  B5BF209257EB6793 CRC64;

  Query Match             2.6%;  Score 8;  DB 1;  Length 80;
  Best Local Similarity   100.0%;  Pred. No. 1.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        256 LALITLGI 263
              ||||||||
Db         12 LALITLGI 19


RESULT 2
1C02_GORGO
ID   1C02_GORGO     STANDARD;      PRT;   366 AA.
AC   P30385;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Class I histocompatibility antigen, GOGO-C0201 alpha chain precursor.
OS   Gorilla gorilla gorilla (Lowland gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9595;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92078860; PubMed=1744581;
RA   Lawlor D.A., Warren E., Taylor P., Parham P.;
RT   "Gorilla class I major histocompatibility complex alleles: comparison
RT   to human and chimpanzee class I.";
RL   J. Exp. Med. 174:1491-1509(1991).
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC       immune system.
CC   -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   ---------------------------------------------------------------------
DR   EMBL; X60251; CAA42803.1; -.
DR   PIR; JH0545; JH0545.
DR   HSSP; P30685; 1A9E.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR001039; MHC_I.
DR   Pfam; PF00047; ig; 1.
DR   Pfam; PF00129; MHC_I; 1.
DR   PRINTS; PR01638; MHCCLASSI.
DR   ProDom; PD000050; MHC_I; 1.
DR   SMART; SM00407; IGc1; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   MHC I; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL        1     24       BY SIMILARITY.
FT   CHAIN        25    366       CLASS I HISTOCOMPATIBILITY ANTIGEN,
FT                                GOGO-C0201 ALPHA CHAIN.
FT   DOMAIN       25    114       EXTRACELLULAR ALPHA-1.
FT   DOMAIN      115    206       EXTRACELLULAR ALPHA-2.
FT   DOMAIN      207    298       EXTRACELLULAR ALPHA-3.
FT   DOMAIN      299    308       CONNECTING PEPTIDE.
FT   TRANSMEM    309    333
FT   DOMAIN      334    366       CYTOPLASMIC TAIL.
FT   DISULFID    125    188       BY SIMILARITY.
FT   DISULFID    227    283       BY SIMILARITY.
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (BY SIMILARITY).
SQ   SEQUENCE   366 AA;  40954 MW;  05E159364C769FC5 CRC64;

  Query Match             2.6%;  Score 8;  DB 1;  Length 366;
  Best Local Similarity   100.0%;  Pred. No. 5.5;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        249 VLVVLAVL 256
              ||||||||
Db        317 VLVVLAVL 324


RESULT 3
1C03_GORGO
ID   1C03_GORGO     STANDARD;      PRT;   366 AA.
AC   P30386;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-APR-1993 (Rel. 25, Last annotation update)
DE   Class I histocompatibility antigen, GOGO-C0202 alpha chain precursor.
OS   Gorilla gorilla gorilla (Lowland gorilla).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX   NCBI_TaxID=9595;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92078860; PubMed=1744581;
RA   Lawlor D.A., Warren E., Taylor P., Parham P.;
RT   "Gorilla class I major histocompatibility complex alleles: comparison
RT   to human and chimpanzee class I.";
RL   J. Exp. Med. 174:1491-1509(1991).
CC   -!- FUNCTION: Involved in the presentation of foreign antigens to the
CC       immune system.
CC   -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
CC       microglobulin).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:20:04 ; Search time 18 Seconds
(without alignments)
896.764 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	2.6	80	1	TX3A_PHONI	P81793 phoneutria
2	8	2.6	366	1	1C02_GORGO	P30385 gorilla gor
3	8	2.6	366	1	1C03_GORGO	P30386 gorilla gor
4	8	2.6	366	1	1C04_GORGO	P30387 gorilla gor
5	8	2.6	366	1	1C07_HUMAN	P10321 homo sapien
6	8	2.6	366	1	1C18_HUMAN	Q29865 homo sapien
7	8	2.6	435	1	YGIK_SALTY	P40800 salmonella
8	7	2.3	161	1	TATB_STRCO	Q9fbk8 streptomyce
9	7	2.3	224	1	XLR1_MOUSE	Q9z114 mus musculu
10	7	2.3	242	1	RS2_SHEON	Q8egh5 shewanella
11	7	2.3	244	1	TNFC_HUMAN	Q06643 homo sapien
12	7	2.3	244	1	TNFC_PANTR	Q862z7 pan troglod
13	7	2.3	302	1	HTPX_AQUAE	O67798 aquifex aeo
14	7	2.3	306	1	TNFC_MOUSE	P41155 mus musculu
15	7	2.3	310	1	TNFC_MARMO	Q9jm10 marmota mon
16	7	2.3	333	1	GPR8_HUMAN	P48146 homo sapien
17	7	2.3	343	1	HMD_METVO	Q50840 methanococc
18	7	2.3	374	1	TRM1_SULTO	Q971v9 sulfolobus
19	7	2.3	403	1	TYRP_ECOLI	P18199 escherichia
20	7	2.3	417	1	PVR_CERAE	P32506 cercopithec
21	7	2.3	417	1	PVR_HUMAN	P15151 homo sapien
22	7	2.3	418	1	SYTF_MOUSE	Q8c6n3 mus musculu
23	7	2.3	454	1	APY_SOLTU	P80595 solanum tub
24	7	2.3	481	1	LMRA_STRLN	P46104 streptomyce
25	7	2.3	491	1	CPB4_RABIT	P00178 oryctolagus
26	7	2.3	491	1	CPB5_RABIT	P12789 oryctolagus
27	7	2.3	524	1	GTR2_HUMAN	P11168 homo sapien
28	7	2.3	574	1	IRL2_MOUSE	Q9ers7 mus musculu
29	7	2.3	595	1	IF2P_ARCFU	O29490 archaeoglob
30	7	2.3	617	1	PYS1_PSEAE	Q06583 pseudomonas
31	7	2.3	643	1	S212_HUMAN	Q92959 homo sapien
32	7	2.3	643	1	S212_MOUSE	Q9ept5 mus musculu
33	7	2.3	643	1	S212_RAT	Q00910 rattus norv
34	7	2.3	688	1	PYS2_PSEAE	Q06584 pseudomonas
35	7	2.3	693	1	NCPR_ASPNG	Q00141 aspergillus
36	7	2.3	697	1	TGM2_CHICK	Q01841 gallus gall
37	7	2.3	721	1	YJIY_ECOLI	P39396 escherichia
38	7	2.3	729	1	GOA5_MOUSE	Q9qye6 mus musculu
39	7	2.3	758	1	SC18_YEAST	P18759 saccharomyc
40	7	2.3	840	1	CC16_YEAST	P09798 saccharomyc
41	7	2.3	909	1	RPS2_ARATH	Q42484 arabidopsis
42	7	2.3	981	1	SCA4_RICFE	Q9aj37 rickettsia
43	7	2.3	987	1	K6P1_CANAL	O94201 candida alb
44	7	2.3	991	1	SCA4_RICSI	Q9aj77 rickettsia
45	7	2.3	1011	1	SCA4_RICAF	Q9aj83 rickettsia
46	7	2.3	1011	1	SCA4_RICMN	Q9aj82 rickettsia
47	7	2.3	1012	1	SCA4_RICSL	Q9aj80 rickettsia
48	7	2.3	1013	1	SCA4_RICRH	Q9aj81 rickettsia
49	7	2.3	1018	1	SCA4_RICJA	Q9aj79 rickettsia
50	7	2.3	1022	1	SCA4_RICCN	Q52658 rickettsia
51	7	2.3	1053	1	ITA3_MOUSE	Q62470 mus musculu
52	7	2.3	1066	1	ITA3_CRISP	P17852 cricetidae
53	7	2.3	1066	1	ITA3_HUMAN	P26006 homo sapien
54	7	2.3	1105	1	YEGE_ECOLI	P38097 escherichia
55	7	2.3	1126	1	HPS5_MOUSE	P59438 mus musculu
56	7	2.3	1142	1	PAK1_YEAST	P38990 saccharomyc
57	7	2.3	1169	1	EX5B_BORBU	O51578 borrelia bu
58	7	2.3	1234	1	YNX5_CAEEL	P34578 caenorhabdi
59	7	2.3	4684	1	PLE1_HUMAN	Q15149 homo sapien
60	7	2.3	5065	1	EPPL_HUMAN	P58107 homo sapien
61	6	1.9	38	1	CRS3_NOTGO	P15534 nototodarus
62	6	1.9	46	1	LHA1_ECTHA	P80100 ectothiorho
63	6	1.9	57	1	ANDP_DROMA	O16825 drosophila
64	6	1.9	57	1	ANDP_DROME	P21663 drosophila
65	6	1.9	57	1	ANDP_DROSE	Q8wsv2 drosophila
66	6	1.9	57	1	YI60_ARCFU	O28419 archaeoglob
67	6	1.9	60	1	ANDP_DROSI	Q8wsv4 drosophila
68	6	1.9	61	1	RS14_MYCGA	O52345 mycoplasma
69	6	1.9	64	1	YDT6_SCHPO	O14211 schizosacch
70	6	1.9	69	1	BR1P_RANPI	Q8qfq5 rana pipien
71	6	1.9	74	1	SRP_SOYBN	Q07502 glycine max
72	6	1.9	76	1	SECG_BACSU	O32233 bacillus su
73	6	1.9	82	1	TX32_PHONI	O76201 phoneutria
74	6	1.9	83	1	TX31_PHONI	O76200 phoneutria
75	6	1.9	86	1	PTHP_STRMU	P45596 streptococc
76	6	1.9	87	1	PTHP_BACHD	Q9k8d2 bacillus ha
77	6	1.9	87	1	PTHP_STRBO	Q9wxk8 streptococc
78	6	1.9	87	1	PTHP_STRSL	P24366 streptococc
79	6	1.9	94	1	YE23_HAEIN	P44194 haemophilus
80	6	1.9	96	1	FER1_AQUAE	O67065 aquifex aeo
81	6	1.9	99	1	YO10_BPHP1	P51712 bacteriopha
82	6	1.9	102	1	KCRB_PIG	Q29594 sus scrofa
83	6	1.9	109	1	V42_BPT3	P20316 bacteriopha
84	6	1.9	115	1	NRG4_MOUSE	Q9wtx4 mus musculu
85	6	1.9	115	1	NU3M_DUGDU	Q8w9m9 dugong dugo
86	6	1.9	115	1	TKN1_RABIT	P41540 oryctolagus
87	6	1.9	118	1	YKD7_YEAST	P32858 saccharomyc
88	6	1.9	119	1	B2MG_HUMAN	P01884 homo sapien
89	6	1.9	119	1	B2MG_MACFA	Q8spw0 macaca fasc
90	6	1.9	119	1	B2MG_PONPY	P16213 pongo pygma
91	6	1.9	123	1	Y055_MYCGE	P47301 mycoplasma
92	6	1.9	123	1	YM82_DEIRA	Q9rs45 deinococcus
93	6	1.9	124	1	SPEH_THETN	Q8ra74 thermoanaer
94	6	1.9	125	1	FRDD_MYCTU	Q10763 mycobacteri
95	6	1.9	130	1	DHSC_PARDE	Q59659 paracoccus
96	6	1.9	130	1	KV5G_MOUSE	P01639 mus musculu
97	6	1.9	130	1	Y06O_BPT4	P39222 bacteriopha
98	6	1.9	130	1	YFFQ_ECOLI	P76548 escherichia
99	6	1.9	132	1	YBFJ_BACSU	O31451 bacillus su
100	6	1.9	134	1	YFID_BACSU	P54720 bacillus su

ALIGNMENTS

RESULT 1

ALIGNMENTS

RESULT 1
I68750
MHC class I lymphocyte antigen - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 21-Jan-2000
C;Accession: I68750
R;Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A;Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-B a
A;Reference number: I54457; MUID:89233295; PMID:2714852
A;Accession: I68750
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-290 <RES>
A;Cross-references: GB:M28207; NID:g576478; PIDN:AAA53259.1; PID:g576479
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;144-209/Domain: immunoglobulin homology <IMM>

Query Match 2.6%; Score 8; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256
||||||||
Db 241 VLVVLAVL 248

RESULT 2
A86406
probable RING zinc finger protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: A86406
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A86406
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-336 <STO>
A;Cross-references: GB:AE005172; NID:g11024872; PIDN:AAG26956.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 2.6%; Score 8; DB 2; Length 336;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 250 LVVLAVLA 257
||||||||
Db 28 LVVLAVLA 35

RESULT 3
HLHUC4
MHC class I histocompatibility antigen HLA-C4 alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 22-Jun-1999
C;Accession: A24512
R;Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.
J. Biol. Chem. 260, 13414-13423, 1985
A;Title: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonuc
A;Reference number: A92500; MUID:86033791; PMID:3863816
A;Accession: A24512
A;Molecule type: DNA
A;Residues: 1-342 <DAV>
A;Cross-references: GB:M11886; NID:g184173; PIDN:AAA52665.1; PID:g386777
C;Genetics:
A;Gene: GDB:HLA-C
A;Cross-references: GDB:119311; OMIM:142840
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F;196-261/Domain: immunoglobulin homology <IMM>
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.6%; Score 8; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 249 VLVVLAVL 256
||||||||
Db 293 VLVVLAVL 300

RESULT 4
E82933
type I restriction enzyme M protein, truncated homolog UU098 [imported] - Ureaplasma ure
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 21-Oct-2002
C;Accession: E82933
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir
A;Reference number: A82870
A;Accession: E82933
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <GLA>
A;Cross-references: GB:AE002110; GB:AF222894; NID:g6899051; PIDN:AAF30504.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: hsdM-1; UU098
A;Genetic code: SGC3
C;Superfamily: type I site-specific deoxyribonuclease chain hsdM

Query Match 2.6%; Score 8; DB 2; Length 348;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 123 RKEIDEIV 130
||||||||
Db 336 RKEIDEIV 343

RESULT 5
JH0546
class I histocompatibility antigen Gogo-C0202 heavy chain precursor - lowland gorilla
C;Species: Gorilla gorilla gorilla (lowland gorilla)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: JH0546
R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human a
A;Reference number: JH0534; MUID:92078860; PMID:1744581
A;Accession: JH0546
A;Molecule type: DNA
A;Residues: 1-366 <LAW>
A;Cross-references: EMBL:X60249; NID:g22882; PIDN:CAA42801.1; PID:g22883
A;Experimental source: EBV-transformed B cell
C;Genetics:
A;Introns: 25/1; 115/1; 207/1; 299/1; 339/1; 350/1; 366/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:21:09 ; Search time 21 Seconds
(without alignments)
1419.970 Million cell updates/sec

Title: US-09-831-805A-6
Perfect score: 310
Sequence: 1 MALRRPPRLRLCARLPDFFL.....VNYIRTDEEGDFRHKSSFVI 310

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

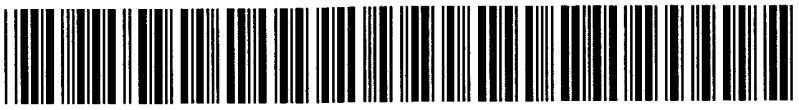
Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8	2.6	290	2	I68750	MHC class I lympho
2	8	2.6	336	2	A86406	probable RING zinc
3	8	2.6	342	1	HLHUC4	MHC class I histoc
4	8	2.6	348	2	E82933	type I restriction
5	8	2.6	366	2	JH0546	class I histocompa
6	8	2.6	366	2	JH0547	class I histocompa
7	8	2.6	366	2	JH0545	class I histocompa
8	8	2.6	366	2	I37078	HLA-C alpha chain
9	8	2.6	492	2	AB1013	probable membrane
10	8	2.6	784	2	A86676	carbon starvation
11	7	2.3	77	2	JC5645	lymphotoxin beta -
12	7	2.3	113	2	AH1748	hypothetical prote
13	7	2.3	171	2	G70548	hypothetical prote
14	7	2.3	172	2	T08548	hypothetical prote
15	7	2.3	173	2	T01282	hypothetical prote
16	7	2.3	173	2	B90241	hypothetical prote
17	7	2.3	173	2	T25730	hypothetical prote
18	7	2.3	177	2	E85833	partial probable s
19	7	2.3	177	2	B90988	partial probable s
20	7	2.3	208	2	T03627	GTP-binding protei
21	7	2.3	208	2	T01588	GTP-binding protei
22	7	2.3	211	2	E86888	hypothetical prote
23	7	2.3	214	2	T47268	phosphatidylserine
24	7	2.3	217	2	T30446	occlusion-derived
25	7	2.3	242	2	G84315	cobalt transport p
26	7	2.3	244	2	A46066	lymphotoxin beta -
27	7	2.3	255	2	T35883	transcription regu
28	7	2.3	280	2	PH0269	epidermal autoanti
29	7	2.3	294	2	H84023	phosphate ABC tran
30	7	2.3	297	2	AB3037	hypothetical prote
31	7	2.3	297	2	A81002	conserved hypothet
32	7	2.3	299	2	A98249	nitrate transport
33	7	2.3	300	2	A82017	probable lipoprote
34	7	2.3	302	2	B70471	heat shock protein
35	7	2.3	306	2	I49139	lymphotoxin-beta -
36	7	2.3	314	2	AG3093	hypothetical prote
37	7	2.3	314	2	C98193	sugar transport sy
38	7	2.3	324	2	T27302	hypothetical prote
39	7	2.3	333	2	I38974	G protein-coupled
40	7	2.3	343	2	H95879	probable sugar ABC
41	7	2.3	346	2	D75303	conserved hypothet
42	7	2.3	362	2	G75614	GGDEF family prote
43	7	2.3	375	2	T46378	hypothetical prote
44	7	2.3	376	2	F71815	hypothetical prote
45	7	2.3	380	2	E88421	protein R74.2 [imp
46	7	2.3	382	2	T24963	hypothetical prote
47	7	2.3	391	2	E72539	hypothetical prote
48	7	2.3	392	1	RWHUPD	poliovirus recepto
49	7	2.3	392	2	B44194	poliovirus recepto
50	7	2.3	400	2	T24258	hypothetical prote
51	7	2.3	402	2	T04348	endosperm specific
52	7	2.3	402	2	G83367	hypothetical prote
53	7	2.3	403	1	GRECY	tyrosine-specific
54	7	2.3	403	2	G90955	tyrosine-specific
55	7	2.3	403	2	D85804	tyrosine-specific
56	7	2.3	417	1	RWHUPA	poliovirus recepto
57	7	2.3	417	2	A44194	poliovirus recepto
58	7	2.3	420	2	T36532	probable membrane
59	7	2.3	421	2	H86217	protein T27G7.16 [
60	7	2.3	431	2	D81282	probable efflux pr
61	7	2.3	437	2	AE1849	proton/sodium-glut
62	7	2.3	454	2	JC4616	apyrase (EC 3.6.1.
63	7	2.3	463	2	D84065	glucose-1-phosphat
64	7	2.3	481	2	S69808	lincomycin resista
65	7	2.3	490	2	A96556	probable tRNA-guan
66	7	2.3	491	1	O4RBPC	cytochrome P450 2B
67	7	2.3	491	2	S31277	cytochrome P450 2B
68	7	2.3	491	2	S31278	cytochrome P450 2B
69	7	2.3	491	2	S35666	cytochrome P450 2B
70	7	2.3	503	2	E83490	probable MFS trans
71	7	2.3	504	2	E87628	hypothetical prote
72	7	2.3	523	2	B95922	hypothetical nucle
73	7	2.3	524	2	A31318	glucose transporte
74	7	2.3	530	2	C95268	probable ABC trans
75	7	2.3	558	2	B87098	conserved hypothet
76	7	2.3	558	2	G70879	hypothetical prote
77	7	2.3	595	2	H69345	translation initia
78	7	2.3	618	2	A36907	pyocin S1 S1A subu
79	7	2.3	629	2	AD1838	Na+/H+ antiporter
80	7	2.3	643	2	A41120	prostaglandin tran
81	7	2.3	671	2	PH0268	epidermal autoanti
82	7	2.3	688	2	H83070	conserved hypothet
83	7	2.3	689	2	D83501	pyocin S2 PA1150 [
84	7	2.3	690	2	C36907	pyocin S2 S2A subu
85	7	2.3	693	1	S38427	NADPH-ferrihemopro
86	7	2.3	698	1	A47203	protein-glutamine
87	7	2.3	705	2	T16088	hypothetical prote
88	7	2.3	709	2	C87258	fatty oxidation co
89	7	2.3	716	2	AB1070	probable carbon st
90	7	2.3	721	2	S56580	carbon starvation
91	7	2.3	721	2	A98293	probable carbon st
92	7	2.3	721	2	D86134	probable carbon st
93	7	2.3	741	2	H90607	atp-dependent heli
94	7	2.3	747	2	T40728	hypothetical prote
95	7	2.3	758	1	S45477	SEC18 protein - ye
96	7	2.3	780	2	T29580	hypothetical prote
97	7	2.3	788	2	T44262	transducer protein
98	7	2.3	789	2	E84236	Htr6 transducer [i
99	7	2.3	798	2	T48304	hypothetical prote
100	7	2.3	815	2	H96494	protein F7F22.2 [i

US 098318050SP1



Creation date: 06-11-2004
Indexing Officer: SUK - SOPHY UK
Team: OIPEBackFileIndexing
Dossier: 09831805

Legal Date: 06-07-2004

No.	Doccode	Number of pages
1	SRNT	2

Total number of pages: 2

Remarks:

Order of re-scan issued on .....